

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 18:48:47 ; Search time 110.978 Seconds
(without alignments)
426.682 Million cell updates/sec

Title: US-10-010-942B-2
Perfect score: 692
Sequence: 1 MMSPAQFLFLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 8 | | | | | | | |
|--------|-------|-------|--------|----|----------|-------------|-----------|
| Result | Query | | | | | | |
| No. | Score | Match | Length | DB | ID | Description | |
| 1 | 692 | 100.0 | 132 | 5 | ABG76923 | Abg76923 | Mouse 3D6 |
| 2 | 655 | 94.7 | 238 | 8 | ADM72033 | Adm72033 | Chimeric |
| 3 | 653 | 94.4 | 238 | 8 | ADP45549 | Adp45549 | Mouse bin |
| 4 | 650 | 93.9 | 135 | 5 | ABB79729 | Abb79729 | Anti-Stre |
| 5 | 644 | 93.1 | 239 | 6 | ABP58274 | Abp58274 | Humanised |
| 6 | 641 | 92.6 | 132 | 2 | AAR12361 | Aar12361 | Light (ka |
| 7 | 641 | 92.6 | 133 | 8 | ADO00819 | Ado00819 | Antibody |
| 8 | 641 | 92.6 | 133 | 8 | ADO43845 | Ado43845 | Light cha |
| 9 | 640 | 92.5 | 132 | 5 | ABG76925 | Abg76925 | Humanised |

| | | | | | | | |
|----|-----|------|-----|---|----------|----------|-----------|
| 10 | 639 | 92.3 | 131 | 2 | AAR12239 | Aar12239 | Mouse MAb |
| 11 | 636 | 91.9 | 132 | 6 | ABG74244 | Abg74244 | Mouse ant |
| 12 | 630 | 91.0 | 132 | 5 | ABG76931 | Abg76931 | Humanised |
| 13 | 628 | 90.8 | 132 | 2 | AAR24712 | Aar24712 | Sequence |
| 14 | 606 | 87.6 | 142 | 4 | AAE07032 | Aae07032 | Murine an |
| 15 | 595 | 86.0 | 239 | 2 | AAR24811 | Aar24811 | Sequence |
| 16 | 589 | 85.1 | 239 | 7 | ADD47025 | Add47025 | Rat Prote |
| 17 | 571 | 82.5 | 113 | 4 | AAE03751 | Aae03751 | Murine PS |
| 18 | 571 | 82.5 | 218 | 4 | AAE03756 | Aae03756 | Chimeric |
| 19 | 566 | 81.8 | 113 | 8 | ADG25828 | Adg25828 | Anti-CD30 |
| 20 | 566 | 81.8 | 114 | 8 | ADG25839 | Adg25839 | Anti-CD30 |
| 21 | 562 | 81.2 | 353 | 2 | AAY06273 | Aay06273 | Anti Fc a |
| 22 | 560 | 80.9 | 112 | 4 | AAE06946 | Aae06946 | Murine 1D |
| 23 | 560 | 80.9 | 112 | 4 | AAU09918 | Aau09918 | Murine mA |
| 24 | 560 | 80.9 | 112 | 5 | ABG75527 | Abg75527 | Mouse mAb |
| 25 | 560 | 80.9 | 112 | 5 | ADF98231 | Adf98231 | Murine mA |
| 26 | 560 | 80.9 | 112 | 7 | ABR61865 | Abr61865 | Mouse MAb |
| 27 | 560 | 80.9 | 112 | 8 | ADQ31246 | Adq31246 | Murine 1A |
| 28 | 560 | 80.9 | 122 | 8 | ADJ95990 | Adj95990 | Immunoglo |
| 29 | 560 | 80.9 | 130 | 8 | ADJ95992 | Adj95992 | Immunoglo |
| 30 | 560 | 80.9 | 238 | 8 | ADM72035 | Adm72035 | Chimeric |
| 31 | 560 | 80.9 | 257 | 3 | AAB09777 | Aab09777 | Antiviral |
| 32 | 559 | 80.8 | 112 | 2 | AAY52765 | Aay52765 | Anti-tiss |
| 33 | 559 | 80.8 | 112 | 2 | AAY52766 | Aay52766 | Anti-tiss |
| 34 | 556 | 80.3 | 112 | 4 | AAE06991 | Aae06991 | Human kap |
| 35 | 555 | 80.2 | 112 | 5 | AAO14971 | Aao14971 | Mouse lig |
| 36 | 550 | 79.5 | 243 | 2 | AAW60769 | Aaw60769 | Single ch |
| 37 | 548 | 79.2 | 112 | 2 | AAW48248 | Aaw48248 | A77 anti- |
| 38 | 548 | 79.2 | 112 | 4 | AAB74621 | Aab74621 | A77 anti- |
| 39 | 548 | 79.2 | 112 | 4 | AAE08554 | Aae08554 | Murine A7 |
| 40 | 548 | 79.2 | 535 | 2 | AAW28491 | Aaw28491 | Human p53 |
| 41 | 548 | 79.2 | 535 | 2 | AAW28492 | Aaw28492 | Human p53 |
| 42 | 547 | 79.0 | 162 | 7 | ADE06760 | Ade06760 | D13 light |
| 43 | 546 | 78.9 | 112 | 7 | ABR62960 | Abr62960 | Monoclona |
| 44 | 543 | 78.5 | 113 | 6 | ABP58270 | Abp58270 | Humanised |
| 45 | 543 | 78.5 | 219 | 6 | ABP58272 | Abp58272 | Humanised |

ALIGNMENTS

RESULT 1

ABG76923

ID ABG76923 standard; protein; 132 AA.

XX

AC ABG76923;

XX

DT 05-NOV-2002 (first entry)

XX

DE Mouse 3D6 VL protein.

XX

KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;

KW variable region complementarity determining region; 3D6; 10D5;

KW variable framework region; amyloidogenic disease; Alzheimer's disease;

KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;

KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;

KW Abeta.

XX
 OS Mus musculus.
 XX
 PN WO200246237-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 06-DEC-2001; 2001WO-US046587.
 XX
 PR 06-DEC-2000; 2000US-0251892P.
 XX
 PA (NEUR-) NEURALAB LTD.
 PA (AMHP) WYETH.
 XX
 PI Basi G, Saldanha J, Yednock T;
 XX
 DR WPI; 2002-519658/55.
 DR N-PSDB; ABS59426.
 XX
 PT Novel light/heavy chain of humanized immunoglobulin for treating
 PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
 PT determining regions and variable framework region from human acceptor
 PT immunoglobulin.
 XX
 PS Claim 67; Fig 1; 171pp; English.
 XX
 CC The present invention relates to new humanized immunoglobulin (Ig) light
 CC chain (LC) or heavy chain (HC) comprising variable region complementarity
 CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
 CC and variable framework region from human acceptor Ig LC or HC sequence.
 CC The invention is useful for preventing or treating an amyloidogenic
 CC disease or Alzheimer's disease in a patient. The invention is also useful
 CC for in vivo imaging amyloid deposits in a patient. The present amino acid
 CC sequence represents a mouse 3D6/10D5 variable light (VL) chain or
 CC variable heavy (VH) chain protein of the invention
 XX
 SQ Sequence 132 AA;

Query Match 100.0%; Score 692; DB 5; Length 132;
 Best Local Similarity 100.0%; Pred. No. 6e-55;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MMSPAQFLFLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW 60
 Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGT HFP 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGT HFP 120
 Qy 121 RTFGGGTKLEIK 132
 |||||||||
 Db 121 RTFGGGTKLEIK 132

RESULT 2
 ADM72033

ID ADM72033 standard; protein; 238 AA.
 XX
 AC ADM72033;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Chimeric mouse-human antibody M3C11 light chain.
 XX
 KW GPC3; glypican 3; anti-GPC3 antibody; cell disruption; anti-cancer;
 KW cytostatic; M3C11.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 PN WO2004022739-A1.
 XX
 PD 18-MAR-2004.
 XX
 PF 04-SEP-2003; 2003WO-JP011318.
 XX
 PR 04-SEP-2002; 2002WO-JP008999.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Aburatani H, Midorikawa Y, Nakano K, Ohizumi I, Ito Y, Tokita S;
 XX
 DR WPI; 2004-269573/25.
 DR N-PSDB; ADM72032.
 XX
 PT Antibody against the N terminus of glypican 3(GPC3) causes cell
 PT disruption and is useful as an anticancer agent.
 XX
 PS Example 4; SEQ ID NO 18; 122pp; Japanese.
 XX
 CC The invention relates to an antibody against the N terminus of glypican 3
 CC (GPC3). The antibody can be used for causing cell disruption and can be
 CC uses as an anti-cancer agent. The present sequence represents a chimeric
 CC mouse-human antibody M3C11 light chain.
 XX
 SQ Sequence 238 AA;

Query Match 94.7%; Score 655; DB 8; Length 238;
 Best Local Similarity 94.7%; Pred. No. 2.6e-51;
 Matches 124; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLLVLWIRETNGYVVMQTPLTLSTIGQPASISCKSSQSLLSDGKTYLNWL 61
 |||
 Db 1 MSPAQFLFLLVLWIRETNGDVVMQTPLTLSTIGQPASISCKSSQSLLSDGKTYLNWL 60
 Qy 62 LQRPQGSPKRLLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTFFPR 121
 |||
 Db 61 LQRPQGSPKRLLIYLVSKLDSGAPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTFFPL 120
 Qy 122 TFGGGTKLEIK 132
 |||
 Db 121 TFGAGTKLELK 131

RESULT 3

ADP45549

ID ADP45549 standard; protein; 238 AA.

XX

AC ADP45549;

XX

DT 09-SEP-2004 (first entry)

XX

DE Mouse binding molecule 11C7 light chain SEQ ID NO:3.

XX

KW binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;

KW nerve repair; neuroprotective; gene therapy;

KW central nervous system injury; CNS injury; neurodegenerative disorder;

KW mouse; antibody.

XX

OS Mus musculus.

XX

PN WO2004052932-A2.

XX

PD 24-JUN-2004.

XX

PF 09-DEC-2003; 2003WO-EP013960.

XX

PR 10-DEC-2002; 2002GB-00028832.

XX

PA (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS PHARMA GMBH.

PA (UYZU-) UNIV ZUERICH.

XX

PI Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;

PI Zurini M;

XX

DR WPI; 2004-468818/44.

XX

PT New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-

PT D20 or NogoA623-640, useful in preparing a composition for treating CNS

PT injury or neurodegenerative disorders.

XX

PS Claim 9; SEQ ID NO 3; 121pp; English.

XX

CC The present invention describes a binding molecule which binds to human
CC NogoA polypeptide, human NiG, human NiG-D20 or human NogoA_623-640 with a
CC dissociation constant of less than 1000nM. Also described: (1) a
CC polynucleotide encoding the binding molecule; (2) an expression vector or
CC system comprising the polynucleotide; (3) a host cell comprising the
CC expression system; (4) a pharmaceutical composition comprising the
CC binding molecule and a carrier or diluent; and (5) treating diseases
CC associated with nerve repair. The binding molecule has neuroprotective
CC activity, and can be used in gene therapy. The binding molecule is useful
CC in preparing a composition for treating central nervous system (CNS)
CC injury or neurodegenerative disorders. The present sequence represents a
CC mouse binding molecule 11C7 light chain, which is used in the
CC exemplification of the present invention.

XX

SQ Sequence 238 AA;

Query Match 94.4%; Score 653; DB 8; Length 238;
Best Local Similarity 93.9%; Pred. No. 4e-51;
Matches 123; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

```
Qy      2 MSPAQFLFLVLWIRETNGYVVMQTPTLTSVTIGQPASISCKSSQSLLDSDGKTYLNWL 61
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MSPAQFLFLVLWIRETSGDVLLTQTPTLTSITIGQPASISCKSSQSLLHSDGKTYLNWL 60

Qy     62 LQRPQGSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPR 121
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     61 LQRPQGSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPQ 120

Qy    122 TFGGGTKLEIK 132
          |||||
Db    121 TFGGGTKLEIK 131
```

RESULT 4

ABB79729

ID ABB79729 standard; protein; 135 AA.

XX

AC ABB79729;

XX

DT 29-OCT-2002 (first entry)

XX

DE Anti-Streptococcus mutans surface antigen MAb SWLA3 VL.

XX

KW Streptococcus mutans; monoclonal antibody; MAb; mouse; chimeric antibody;

KW antibody; anticaries; transgenic plant; transgenic animal; caries;

KW immunotherapy; therapy.

XX

OS Mus musculus.

XX

PN US2002068066-A1.

XX

PD 06-JUN-2002.

XX

PF 15-JUN-2001; 2001US-00881823.

XX

PR 20-AUG-1999; 99US-00378577.

XX

PA (SHIW/) SHI W.

PA (MORR/) MORRISON S L.

PA (TRIN/) TRINH K.

PA (WIMS/) WIMS L.

PA (CHEN/) CHEN L.

PA (ANDE/) ANDERSON M H.

XX

PI Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;

XX

DR WPI; 2002-565838/60.

DR N-PSDB; ABN84610.

XX

PT Treatment and prevention of dental caries in mammals, in particular

PT humans by orally administering genetically engineered or purified

PT antibodies that bind to surface antigens of carcinogenic organisms.

XX
PS Claim 13; Fig 3A; 30pp; English.
XX
CC The present sequence is the protein sequence of the light chain variable
CC region (VL) of the murine monoclonal antibody SWLA3 (IgG), which binds
CC specifically to the surface antigens of cariogenic type c Streptococcus
CC mutans (ATCC 25175). The monoclonal antibody is produced by SWLA3 (ATCC
CC HB 12558) hybridoma cells. In an example from the invention, chimeric
CC monoclonal antibody TEFEE was produced comprising SWLA3 variable regions
CC and human antibody constant regions. Such chimeric monoclonal antibodies
CC can be used to prevent or treat dental caries in humans. The antibodies
CC engage the effector apparatus of the human immune system when they bind
CC cariogenic organisms, resulting in their destruction. The chimeric
CC antibodies may be produced in edible plants, in transgenic animals, or in
CC chicken eggs for oral ingestion
XX
SQ Sequence 135 AA;

Query Match 93.9%; Score 650; DB 5; Length 135;
Best Local Similarity 93.2%; Pred. No. 4e-51;
Matches 123; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

```

Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
        |||:|:|:|
Db      1 MMSPAQFLFLLVLWIRETNGDVVMQTPTPLTSLVTIGQPASISCKSSQSLLDRDGRITYLSW 60

Qy     61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFP 120
        |||:|:|:|
Db     61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTTHFP 120

Qy    121 RTFGGGTKLEIK 132
        ||| |||:|
Db    121 LTFGAGTKLELK 132

```

```

RESULT 5
ABP58274
ID   ABP58274 standard; protein; 239 AA.
XX
AC   ABP58274;
XX
DT   23-OCT-2003   (revised)
DT   31-MAR-2003   (first entry)
XX
DE   Humanised 3D6 antibody light chain.
XX
KW   Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse;
KW   human; humanised antibody; antibody; Alzheimer's disease;
KW   Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Chimeric.
XX
FH   Key                Location/Qualifiers
FT   Peptide            1..20
FT                       /label= Signal peptide

```

FT Protein 21. .239
 FT /label= Mature_peptide
 FT /note= "the mature light chain is claimed in Claim 5"
 FT Region 21. .133
 FT /note= "light chain variable region, claimed in Claim 4"
 FT Region 44. .59
 FT /note= "CDR1"
 FT Region 75. .81
 FT /note= "CDR2"
 FT Region 114. .122
 FT /note= "CDR3"

XX

PN WO200288306-A2.

XX

PD 07-NOV-2002.

XX

PF 26-APR-2002; 2002WO-US011853.

XX

PR 30-APR-2001; 2001US-0287539P.

XX

PA (ELIL) LILLY & CO ELI.

XX

PI Tsurushita N, Vasquez M;

XX

DR WPI; 2003-183835/18.

DR N-PSDB; ABZ24632, ABZ24634.

XX

PT New humanized forms of mouse 3D6 antibodies, useful for treating Down's
 PT syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral
 PT amyloid angiopathy, or for inhibiting formation of or reducing Abeta
 PT plaque in the brain.

XX

PS Disclosure; Page 12-13; 54pp; English.

XX

CC The present sequence is that of a preferred light chain of a humanised
 CC antibody of the present invention. In the variable region of this
 CC sequence, the complementarity determining regions (CDRs) originate from
 CC murine monoclonal antibody 3D6 and the framework region from human
 CC germline Vk segment DPK19 and J segment Jk4. Novel humanised antibodies
 CC of the invention have CDRs from 3D6 and human framework sequences. These
 CC humanised antibodies have binding affinities (affinity and epitope
 CC location) approximately the same as those of the mouse 3D6 antibody. The
 CC invention includes antibodies, single chain antibodies, and their
 CC fragments, as well as nucleotide sequences, vectors, transformed host
 CC cells, and methods of using the humanised antibody to treat, prevent,
 CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology
 CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
 CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
 CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
 CC OS field)

XX

SQ Sequence 239 AA;

Query Match 93.1%; Score 644; DB 6; Length 239;

Best Local Similarity 90.9%; Pred. No. 2.6e-50;

Matches 120; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
 |||||||||||||||| ||||:|:| ||:||||||||||||||||||
 Db 1 MMSPAQFLFLLVLWIRETNGDVMTQSPLSLPVTLGQPASISCKSSQSLLDSDGKTYLNW 60

Qy 61 LLQRPQGQSPKRLLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTFFP 120
 | ||||||:||||||||||||||:||||||||||||||:||||:|:|||||||
 Db 61 LQRPQGQSPRRLLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTFFP 120

Qy 121 RTFGGGTKLEIK 132
 ||||||:|
 Db 121 RTFGGGTKVEIK 132

RESULT 6

AAR12361

ID AAR12361 standard; protein; 132 AA.

XX

AC AAR12361;

XX

DT 25-MAR-2003 (revised)

DT 15-AUG-1991 (first entry)

XX

DE Light (kappa) chain variable region of murine 4D12 immunoglobulin.

XX

KW Chimeric antibodies; immunoconjugates; HIV; AIDS.

XX

OS Mus musculus.

XX

PN WO9107493-A.

XX

PD 30-MAY-1991.

XX

PF 13-NOV-1989; 89US-00433730.

XX

PR 13-NOV-1989; 89US-00433730.

XX

PA (XOMA) XOMA CORP.

PA (GREC) GREEN CROSS CORP.

XX

PI Better MD, Horwitz AH, Ghoshdasti P, Robinson R;

XX

DR WPI; 1991-178105/24.

DR N-PSDB; AAQ12063.

XX

PT New chimeric mouse-human antibodies - used to detect, kill and remove HIV
 PT -1 antigen from sample.

XX

PS Disclosure; Fig 18; 107pp; English.

XX

CC This is the light (kappa) - chain variable (V) region of a mouse
 CC monoclonal antibody (MAb), 4D12, and is specific for an HIV-1 viral
 CC antigen. It is used in the construction of a chimeric MAb comprising
 CC heavy and light chains having murine V regions and human C regions. The
 CC chimeric MAbs are more effective than murine MAb 4D12 since they have an
 CC increased compatibility in humans. The heavy and light chain V-regions
 CC are joined by manipulating their respective joining (J) regions, to
 CC generate restriction enzyme recognition sites. The chimeric MAbs can be

CC used as immunoconjugates, in association with e.g. toxins for HIV
CC treatment. They can also be used in diagnosis of HIV. See also AAQ12056-
CC 62. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003
CC to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)
XX
SQ Sequence 132 AA;

Query Match 92.6%; Score 641; DB 2; Length 132;
Best Local Similarity 90.9%; Pred. No. 2.5e-50;
Matches 120; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
|||||
Db 1 MMSPAQFLFLLVLWIRETNGDVMTQTPLTSLVTIGQPASFCKSSQSLLDSDGKTFLNW 60
Qy 61 LLQRPQGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGYYCWQGTTHFP 120
|||||:|||||:|||||:|||||:|||||
Db 61 FLQRPQGQSPKRLLYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGYYCWQGSHP 120
Qy 121 RTFGGGTKLEIK 132
||| ||||:|
Db 121 ITFGAGTKLELR 132

RESULT 7

ADO00819

ID ADO00819 standard; protein; 133 AA.

XX

AC ADO00819;

XX

DT 01-JUL-2004 (first entry)

XX

DE Antibody JRF/cAbeta40/10 light chain variable region, SEQ ID 6.

XX

KW Neuroprotective; Nootropic; Haemostatic; Vaccine; Amyloid-beta 11;

KW beta-amyloid-related disease; Alzheimer's disease; Abeta secretase;

KW cleavage site; immunogen; murine; antibody; light chain; variable region;

KW JRF/cAbeta40/10.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT Domain 44. .59

FT /note= "CDR1"

FT Domain 75. .81

FT /note= "CDR2"

FT Domain 114. .122

FT /note= "CDR3"

XX

PN WO2004029629-A1.

XX

PD 08-APR-2004.

XX

PF 27-SEP-2002; 2002WO-EP011062.

XX

PR 27-SEP-2002; 2002WO-EP011062.

XX

PA (JANC) JANSSEN PHARM NV.
 XX
 PI Mercken MH, Vandermeeren MMPP;
 XX
 DR WPI; 2004-316180/29.
 XX
 PT New N-11 truncated amyloid-beta monoclonal antibodies specific for human
 PT Amyloid-beta 11 N-terminal site (A-beta11-x peptides), useful for
 PT diagnosing or treating beta-amyloid-related diseases e.g. Alzheimer's
 PT disease.
 XX
 PS Disclosure; SEQ ID NO 6; 42pp; English.
 XX
 CC The present invention relates to an antibody expressed by the hybridoma
 CC cells J&JPRD/hAbeta11/1 and J&JPRD/hAbeta11/2, which is capable of
 CC specifically recognizing human Amyloid-beta 11 N-terminal site (i.e.,
 CC Abeta11-x peptides). The antibody is useful for diagnosing beta-amyloid-
 CC related diseases. It is particularly useful for prognosing and monitoring
 CC response to therapy of Alzheimer's disease and other beta-amyloid related
 CC diseases and in passive immunization as a method for treating such
 CC diseases. A humanized form of the antibody is useful for manufacturing a
 CC medicament for treating, preventing or reversing cognitive decline in
 CC clinical or pre-clinical Alzheimer's Disease, Down's syndrome, Hereditary
 CC Cerebral Hemorrhage with Amyloidosis of the Dutch-Type, cerebral amyloid
 CC angiopathy or other beta-amyloid-related diseases, or to inhibit the
 CC formation of amyloid plaques or the effects of toxic soluble Amyloid-beta
 CC ; species in humans. It can also be used in assay systems such as
 CC competitive methods and nephelometry. The present sequence was used to
 CC illustrate the invention.
 XX
 SQ Sequence 133 AA;

Query Match 92.6%; Score 641; DB 8; Length 133;
 Best Local Similarity 91.7%; Pred. No. 2.6e-50;
 Matches 121; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLLDSDGKTYLW 60
 ||||||||||||||||| |||||||||:||||||||||| |||| |||||:|
 Db 1 MMSPAQFLFLLVLWIRETNGDVVMQTPTLTLAVTIGQPASISCKSGQSLLARDGKTYLSW 60
 Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFP 120
 |||||||||||||||||||||:|||||||||||:|:|||||:|||||||
 Db 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFSGSGSGTDFTLKINRVEAEDLGVYYCWQGTTHFP 120
 Qy 121 RTFGGGTKLEIK 132
 ||||||| ||||
 Db 121 RTFGGGTNLEIK 132

RESULT 8
 ADO43845
 ID ADO43845 standard; protein; 133 AA.
 XX
 AC ADO43845;
 XX
 DT 15-JUL-2004 (first entry)
 XX

DE Light chain variable region of anti-amyloid-beta antibody.
 XX
 KW antibody; Amyloid-beta11-x peptide; BACE-1; amyloid-beta; beta-secretase;
 KW beta-amyloid precursor protein; beta-amyloid-related disease;
 KW Alzheimer's disease; vaccine; Down's syndrome;
 KW hereditary cerebral haemorrhage; amyloidosis;
 KW cerebral amyloid angiopathy; amyloid plaque.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Region 44. .59
 FT /note= "CDR1"
 FT Region 75. .81
 FT /note= "CDR2"
 FT Region 114. .122
 FT /note= "CDR3"
 XX
 PN WO2004029630-A1.
 XX
 PD 08-APR-2004.
 XX
 PF 09-SEP-2003; 2003WO-EP010092.
 XX
 PR 27-SEP-2002; 2002WO-EP011062.
 XX
 PA (JANC) JANSSEN PHARM NV.
 XX
 PI Mercken MH, Vandermeeren MMPP;
 XX
 DR WPI; 2004-316181/29.
 XX
 PT New N-11 truncated amyloid-beta monoclonal antibodies specific for human
 PT Amyloid-beta 11-x peptides (A-beta11-x peptides), useful for diagnosing
 PT or treating beta-amyloid-related diseases e.g., Alzheimer's disease.
 XX
 PS Disclosure; Page 38-39; 50pp; English.
 XX
 CC The specification describes a monoclonal antibody which specifically
 CC recognizes human Amyloid-beta11-x peptides. These peptides result from
 CC overexpression of BACE-1 which causes additional cleavage at the +11 site
 CC of amyloid-beta, generating shorter fragments known as Amyloid-beta11-x
 CC peptides. BACE-1 is the major beta-secretase required for cleavage of
 CC beta-amyloid precursor protein. The antibody is useful for detecting the
 CC presence of amyloid-beta peptides in a tissue or fluid sample and for
 CC diagnosing beta-amyloid-related diseases. It is particularly useful for
 CC prognosing and monitoring response to therapy of Alzheimer's disease and
 CC other beta-amyloid related diseases and in passive immunization as a
 CC method for treating such diseases. A humanized form of the antibody is
 CC useful for manufacturing a medicament for treating, preventing or
 CC reversing cognitive decline in clinical or pre-clinical Alzheimer's
 CC Disease, Down's syndrome, Hereditary Cerebral Haemorrhage with
 CC Amyloidosis of the Dutch-Type, cerebral amyloid angiopathy or other beta-
 CC amyloid-related diseases, or to inhibit the formation of amyloid plaques
 CC or the effects of toxic soluble Amyloid-beta species in humans. The
 CC present sequence represents the light chain variable region of an
 CC antibody that recognises amyloid-beta-40 and amyloid-beta11-x peptide

CC amyloid-beta11-40.

XX

SQ Sequence 133 AA;

Query Match 92.6%; Score 641; DB 8; Length 133;
Best Local Similarity 91.7%; Pred. No. 2.6e-50;
Matches 121; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 1 | MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSTVIGQPASISCKSSQSLDSDGKTYLNW | 60 |
| | | | |
| Db | 1 | MMSPAQFLFLLVLWIRETNGDVVMQTPLTLAVTIGQPASISCKSGQSLLDGKTYLSW | 60 |
| Qy | 61 | LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP | 120 |
| | | | |
| Db | 61 | LLQRPQGSPKRLIYLVSKLDSGVPDRFSGSGSGTDFTLKINRVEAEDLGYYCWQGTHFP | 120 |
| Qy | 121 | RTFGGGTKLEIK | 132 |
| | | | |
| Db | 121 | RTFGGGTNLEIK | 132 |

RESULT 9

ABG76925

ID ABG76925 standard; protein; 132 AA.

XX

AC ABG76925;

XX

DT 05-NOV-2002 (first entry)

XX

DE Humanised 3D6 light chain variable region #1.

XX

KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;

KW variable region complementarity determining region; 3D6; 10D5;

KW variable framework region; amyloidogenic disease; Alzheimer's disease;

KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;

KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;

KW Abeta.

XX

OS Homo sapiens.

OS Mus musculus.

OS Synthetic.

XX

PN WO200246237-A2.

XX

PD 13-JUN-2002.

XX

PF 06-DEC-2001; 2001WO-US046587.

XX

PR 06-DEC-2000; 2000US-0251892P.

XX

PA (NEUR-) NEURALAB LTD.

PA (AMHP) WYETH.

XX

PI Basi G, Saldanha J, Yednock T;

XX

DR WPI; 2002-519658/55.

XX

XX
 OS Mus sp.
 XX
 PN US2002132983-A1.
 XX
 PD 19-SEP-2002.
 XX
 PF 10-DEC-2001; 2001US-00006773.
 XX
 PR 30-NOV-2000; 2000US-0250087P.
 PR 30-NOV-2000; 2000US-0250089P.
 XX
 PA (JUNG/) JUNGHANS R P.
 XX
 PI Junghans RP;
 XX
 DR WPI; 2003-208946/20.
 DR N-PSDB; ABX16570.
 XX
 PT New chimeric molecule useful in treating patients with disorders, such as
 PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer
 PT comprises GD3 and/or PSMA binding domains of antibody.
 XX
 PS Disclosure; Page 13; 35pp; English.
 XX
 CC The invention relates to a chimaeric molecule comprising the GD3
 CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3
 CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)
 CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
 CC sequences, the zeta signalling chain of the T cell receptor and an
 CC intervening CD8alpha hinge in which cysteine residues have been mutated.
 CC The chimaeric molecules expressed in T cells or NK cells or other
 CC effector cells are useful in treating patients with cancers expressing
 CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
 CC and/or together with each other or with heterologous constructs to engage
 CC additional stimulatory and functional properties of the effector cells to
 CC enhance the antitumour therapeutic efficacy (claimed). They are
 CC particularly useful in disorders including melanoma, neuroendocrine
 CC tumours and prostate and small cell lung cancer. The present sequence
 CC represents the mouse antibody 3D8 light chain variable region
 XX
 SQ Sequence 132 AA;

Query Match 91.9%; Score 636; DB 6; Length 132;
 Best Local Similarity 93.9%; Pred. No. 7.2e-50;
 Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLLDSGKTYLNWL 61
 |||||||||:|||| ||||||||| ||||||||| |||||||||
 Db 1 MSPAQFLFLLVLWIQETNGDVVMTQTPLTSLVTIGQPASISCKSSQSLLYSNGKTYLNWL 60
 Qy 62 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTTHFPR 121
 |||||||||:|||||:|||| |||||
 Db 61 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCVQGTTHFPH 120
 Qy 122 TFGGGTKLEIK 132
 |||||||||

Db 121 TFGGGTKLEIK 131

RESULT 12

ABG76931

ID ABG76931 standard; protein; 132 AA.

XX

AC ABG76931;

XX

DT 05-NOV-2002 (first entry)

XX

DE Humanised 3D6 light chain variable region #2.

XX

KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;

KW variable region complementarity determining region; 3D6; 10D5;

KW variable framework region; amyloidogenic disease; Alzheimer's disease;

KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;

KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;

KW Abeta.

XX

OS Homo sapiens.

OS Mus musculus.

OS Synthetic.

XX

PN WO200246237-A2.

XX

PD 13-JUN-2002.

XX

PF 06-DEC-2001; 2001WO-US046587.

XX

PR 06-DEC-2000; 2000US-0251892P.

XX

PA (NEUR-) NEURALAB LTD.

PA (AMHP) WYETH.

XX

PI Basi G, Saldanha J, Yednock T;

XX

DR WPI; 2002-519658/55.

XX

PT Novel light/heavy chain of humanized immunoglobulin for treating

PT amyloidogenic disease, has 3D6/10D5 variable region complementarity

PT determining regions and variable framework region from human acceptor

PT immunoglobulin.

XX

PS Claim 55; Page 157; 171pp; English.

XX

CC The present invention relates to new humanized immunoglobulin (Ig) light
CC chain (LC) or heavy chain (HC) comprising variable region complementarity
CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
CC and variable framework region from human acceptor Ig LC or HC sequence.

CC The invention is useful for preventing or treating an amyloidogenic
CC disease or Alzheimer's disease in a patient. The invention is also useful
CC for in vivo imaging amyloid deposits in a patient. The present amino acid
CC sequence represents a humanized 3D6 variable light (VL) chain or variable
CC heavy (VH) chain protein of the invention

XX

SQ Sequence 132 AA;

Query Match 91.0%; Score 630; DB 5; Length 132;
Best Local Similarity 89.4%; Pred. No. 2.5e-49;
Matches 118; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

[illegible]

RESULT 13

AAR24712

ID AAR24712 standard; protein; 132 AA.

XX

AC AAR24712;

XX

DT 25-MAR-2003 (revised)

DT 28-DEC-1992 (first entry)

XX

DE Sequence encoded by the genomic FIB1-11 kappa chain variable (VFK) gene.

XX

KW Chimeric monoclonal antibody; anti-fibrin antibody; PCR;

KW antithrombotic agent; myocardial infarction therapy.

XX

OS Mus musculus.

XX

| FH | Key | Location/Qualifiers |
|----|-----|---------------------|
|----|-----|---------------------|

| | | |
|----|---------|--------|
| FT | Peptide | 1. .20 |
|----|---------|--------|

FT /label= leader

| | | |
|----|--------|---------|
| FT | Region | 21. .43 |
|----|--------|---------|

```
FT /label= Framework Region (FR) 1
```

| | | |
|----|--------|---------|
| FT | Region | 44. .59 |
|----|--------|---------|

```
FT /label= complementarity determining region(CDR)1
```

| | | |
|----|--------|---------|
| FT | Region | 60. .74 |
|----|--------|---------|

FT /label= FR-2

| | | |
|----|--------|---------|
| FT | Region | 75. .81 |
|----|--------|---------|

FT /label= CDR-2

| | | | |
|----|--------|-----|------|
| FT | Region | 82. | .112 |
|----|--------|-----|------|

FT /label= FR-3

| | | | |
|----|--------|------|------|
| FT | Region | 113. | .122 |
|----|--------|------|------|

FT /label= CDR-3

| | | | |
|----|--------|------|------|
| FT | Region | 123. | .132 |
|----|--------|------|------|

FT /label= FR-4

XX

PN EP491351-A2.

XX

PD 24-JUN-1992.

XX

PF 17-DEC-1991; 91EP-00121591.

XX
 PR 18-DEC-1990; 90JP-00413829.
 PR 11-NOV-1991; 91JP-00294464.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Iwasa S, Tada H, Watanabe T;
 XX
 DR WPI; 1992-209528/26.
 DR N-PSDB; AAQ25665.
 XX
 PT Chimeric monoclonal antibodies - contain anti-human fibrin antibody light
 PT and heavy chain variable and constant for treating thrombotic conditions
 PT e.g. myocardial infarction.
 XX
 PS Example; Fig 1; 87pp; English.
 XX
 CC A genomic DNA library was prepd. from mouse anti-human fibrin specific
 CC antibody producer hybrid FIB1-11. Screening using a 32P- labeled mouse
 CC JK4-5 gene fragment as a hybridisation probe gave three positive
 CC recombinant phage clones. Phage clone KE14 was identified as a clone
 CC contg. a 15kb fragment coding for the VFK gene. The phage clone KE14 was
 CC subcloned in the plasmid vector pUC119 and sequenced. VFK was a
 CC functional VK gene formed by recombination between the VK gene belonging
 CC to the Subgroup II (VKII) and the JK2 gene (see AAQ25665). (Updated on 25
 CC -MAR-2003 to correct PN field.)
 XX
 SQ Sequence 132 AA;

Query Match 90.8%; Score 628; DB 2; Length 132;
 Best Local Similarity 91.7%; Pred. No. 3.8e-49;
 Matches 121; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLLDSDGKTYLNW 60
 ||||||||||||||||| ||| ||||||||||||| ||| |||||||||||||
 Db 1 MMSPAQFLFLLVLWIRETNGDVVMAQTPTLTLSTIGQPAFISCTSSQSLLDSDGKTYLNW 60
 Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFP 120
 ||||||||||||||||| ||||||||||||| |||||:|:|||||:||||| |||
 Db 61 LLQRPQGSPKRLIYLVSKLYSGVPDRFTGSGSGTAFTLKINRVEAEDLGYYCWQGIHFP 120
 Qy 121 RTFGGGTKLEIK 132
 |||||||||
 Db 121 YTFGGGTKLEIK 132

RESULT 14

AAE07032

ID AAE07032 standard; protein; 142 AA.

XX

AC AAE07032;

XX

DT 16-OCT-2001 (first entry)

XX

DE Murine antibody 1D9 kappa light chain variable region.

XX

KW Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;

KW neuroprotective; immunosuppressive; human immunodeficiency virus;
KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;
KW inflammatory glomerulopathy; vascular intervention;
KW neointimal hyperplasia; antibody 1D9 kappa light chain variable region.

XX
OS Mus sp.

XX
FH Key Location/Qualifiers
FT Peptide 1. .17
FT /label= Signal_peptide
FT Protein 18. .142
FT /note= "Murine mature antibody 1D9 kappa light chain
FT variable region"
FT Region 18. .130
FT /label= Variable_region
FT Region 131. .142
FT /label= Constant_region

XX
PN WO200157226-A1.

XX
PD 09-AUG-2001.

XX
PF 02-FEB-2001; 2001WO-US003537.

XX
PR 03-FEB-2000; 2000US-00497625.

XX
PA (MILL-) MILLENNIUM PHARM INC.

XX
PI Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;

XX
DR WPI; 2001-488888/53.
DR N-PSDB; AAD13177.

XX
PT Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated
PT disorder in a patient, comprises a binding specificity for CCR2, and a
PT non-human antigen binding region and human immunoglobulin.

XX
PS Disclosure; Fig 22; 183pp; English.

XX
CC The patent discloses a humanised antibody or its antigen-binding
CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),
CC comprising an antigen binding region of non-human origin and at least a
CC portion of an immunoglobulin of human origin. The humanised antibodies
CC are useful for inhibiting the interaction of a cell expressing CCR2. They
CC are useful for inhibiting or treating HIV infection. The proteins of the
CC invention are useful for inhibiting leukocyte trafficking, for treating
CC CCR2-mediated disorders such as inflammatory disorder, autoimmune
CC disorders such as rheumatoid arthritis and multiple sclerosis,
CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They
CC are useful in therapy or diagnosis, and in the manufacture of a
CC medicament for treating CCR-2 mediated disease. They are also useful for
CC treating allergy, anaphylaxis, malignancy, chronic and acute
CC inflammation, histamine and IgE- mediated allergic reaction, shock,

CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory
 CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis
 CC associated with vascular intervention, including angioplasty and/or stent
 CC placement in a mammal. Humanised antibodies are also useful for
 CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting
 CC neointimal hyperplasia of a vessel in a mammal, preferably associated
 CC with vascular intervention. The present sequence is murine antibody 1D9
 CC kappa light chain variable region

XX

SQ Sequence 142 AA;

Query Match 87.6%; Score 606; DB 4; Length 142;
 Best Local Similarity 93.5%; Pred. No. 4.1e-47;
 Matches 115; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 10 LLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSP 69
 ||||| | |||||:| |||||:|||||
 Db 7 LLVLWIRETIGDVVMTQTPTLTLSTVGHSPASISCKSSQSLDSDGKTFLNWLLQRPQGSP 66

Qy 70 KRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTFPRTFGGGTKL 129
 |||||:|||||:|||||
 Db 67 KRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHTFPYTFGGGTKL 126

Qy 130 EIK 132
 |||
 Db 127 EIK 129

RESULT 15

AAR24811

ID AAR24811 standard; protein; 239 AA.

XX

AC AAR24811;

XX

DT 25-MAR-2003 (revised)

DT 28-DEC-1992 (first entry)

XX

DE Sequence encoded by the chimeric kappa chain cDNA (lgkv) contained in
 DE pTB1427.

XX

KW Chimeric monoclonal antibody; anti-fibrin antibody; primer;
 KW antithrombotic agent; myocardial infarction therapy.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Peptide 1. .20

FT /label= leader

FT Region 21. .133

FT /label= V-kappa

FT Misc-difference 130

FT /note= "Alternatively = Glu"

FT Region 134. .239

FT /label= C-kappa

XX

PN EP491351-A2.

XX

Search completed: December 13, 2004, 19:13:22
Job time : 113.978 secs

OM protein - protein search, using sw model

Run on: December 13, 2004, 19:05:17 ; Search time 27.3778 Seconds
(without alignments)
319.748 Million cell updates/sec

Title: US-10-010-942B-2
Perfect score: 692
Sequence: 1 MMSPAQFLFLLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| | | Query | | | | | Description |
|--------|-----|-------|-------|--------|----|--------------------|-------------------|
| Result | No. | Score | Match | Length | ID | DB | |
| | 1 | 649 | 93.8 | 131 | 4 | US-09-647-468-163 | Sequence 163, App |
| | 2 | 646 | 93.4 | 131 | 4 | US-09-647-468-164 | Sequence 164, App |
| | 3 | 606 | 87.6 | 142 | 4 | US-09-840-459-102 | Sequence 102, App |
| | 4 | 606 | 87.6 | 142 | 4 | US-09-497-625A-102 | Sequence 102, App |
| | 5 | 562 | 81.2 | 353 | 4 | US-09-203-958A-4 | Sequence 4, Appli |
| | 6 | 560 | 80.9 | 112 | 4 | US-09-809-739-11 | Sequence 11, Appl |
| | 7 | 560 | 80.9 | 112 | 4 | US-09-840-459-9 | Sequence 9, Appli |
| | 8 | 560 | 80.9 | 112 | 4 | US-09-497-625A-9 | Sequence 9, Appli |
| | 9 | 559 | 80.8 | 112 | 4 | US-09-647-468-149 | Sequence 149, App |
| | 10 | 559 | 80.8 | 112 | 4 | US-09-647-468-150 | Sequence 150, App |
| | 11 | 556 | 80.3 | 112 | 4 | US-09-840-459-54 | Sequence 54, Appl |

| | | | | | | |
|----|-----|------|-----|---|--------------------|-------------------|
| 12 | 556 | 80.3 | 112 | 4 | US-09-497-625A-54 | Sequence 54, Appl |
| 13 | 548 | 79.2 | 112 | 2 | US-08-678-194-6 | Sequence 6, Appli |
| 14 | 548 | 79.2 | 112 | 3 | US-08-890-011-6 | Sequence 6, Appli |
| 15 | 548 | 79.2 | 112 | 3 | US-09-262-724-6 | Sequence 6, Appli |
| 16 | 548 | 79.2 | 535 | 3 | US-08-983-035A-38 | Sequence 38, Appl |
| 17 | 538 | 77.7 | 112 | 4 | US-09-809-739-16 | Sequence 16, Appl |
| 18 | 538 | 77.7 | 112 | 4 | US-09-840-459-14 | Sequence 14, Appl |
| 19 | 538 | 77.7 | 112 | 4 | US-09-497-625A-14 | Sequence 14, Appl |
| 20 | 537 | 77.6 | 132 | 1 | US-08-477-877B-91 | Sequence 91, Appl |
| 21 | 537 | 77.6 | 132 | 2 | US-08-472-281A-91 | Sequence 91, Appl |
| 22 | 537 | 77.6 | 132 | 2 | US-08-477-989B-91 | Sequence 91, Appl |
| 23 | 533 | 77.0 | 112 | 4 | US-09-809-739-17 | Sequence 17, Appl |
| 24 | 533 | 77.0 | 112 | 4 | US-09-840-459-15 | Sequence 15, Appl |
| 25 | 533 | 77.0 | 112 | 4 | US-09-497-625A-15 | Sequence 15, Appl |
| 26 | 530 | 76.6 | 112 | 4 | US-09-809-739-15 | Sequence 15, Appl |
| 27 | 530 | 76.6 | 112 | 4 | US-09-840-459-13 | Sequence 13, Appl |
| 28 | 530 | 76.6 | 112 | 4 | US-09-497-625A-13 | Sequence 13, Appl |
| 29 | 527 | 76.2 | 114 | 4 | US-09-840-459-106 | Sequence 106, App |
| 30 | 527 | 76.2 | 114 | 4 | US-09-497-625A-106 | Sequence 106, App |
| 31 | 525 | 75.9 | 112 | 4 | US-09-809-739-18 | Sequence 18, Appl |
| 32 | 525 | 75.9 | 112 | 4 | US-09-840-459-107 | Sequence 107, App |
| 33 | 520 | 75.1 | 112 | 4 | US-09-809-739-14 | Sequence 14, Appl |
| 34 | 520 | 75.1 | 112 | 4 | US-09-840-459-12 | Sequence 12, Appl |
| 35 | 520 | 75.1 | 112 | 4 | US-09-497-625A-12 | Sequence 12, Appl |
| 36 | 518 | 74.9 | 132 | 1 | US-08-477-877B-84 | Sequence 84, Appl |
| 37 | 518 | 74.9 | 132 | 2 | US-08-472-281A-84 | Sequence 84, Appl |
| 38 | 518 | 74.9 | 132 | 2 | US-08-477-989B-84 | Sequence 84, Appl |
| 39 | 515 | 74.4 | 100 | 4 | US-09-840-459-22 | Sequence 22, Appl |
| 40 | 515 | 74.4 | 100 | 4 | US-09-497-625A-22 | Sequence 22, Appl |
| 41 | 515 | 74.4 | 135 | 1 | US-08-259-372A-12 | Sequence 12, Appl |
| 42 | 515 | 74.4 | 135 | 1 | US-08-468-671-12 | Sequence 12, Appl |
| 43 | 512 | 74.0 | 112 | 3 | US-09-184-658-49 | Sequence 49, Appl |
| 44 | 512 | 74.0 | 112 | 4 | US-09-504-262D-49 | Sequence 49, Appl |
| 45 | 508 | 73.4 | 289 | 3 | US-09-184-658-63 | Sequence 63, Appl |

ALIGNMENTS

RESULT 1

US-09-647-468-163

; Sequence 163, Application US/09647468

; Patent No. 6677436

; GENERAL INFORMATION:

; APPLICANT: SATO, KOH

; APPLICANT: ADACHI, HIDEKI

; APPLICANT: YABUTA, NAOHIRO

; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND

; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY

; FILE REFERENCE: 053466/0289

; CURRENT APPLICATION NUMBER: US/09/647,468

; CURRENT FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: PCT/JP99/01768

; PRIOR FILING DATE: 1999-04-02

; PRIOR APPLICATION NUMBER: JP 10-91850

; PRIOR FILING DATE: 1998-04-03

; NUMBER OF SEQ ID NOS: 183

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence coding for L chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-7
US-09-647-468-163
```

```
Query Match          93.8%; Score 649; DB 4; Length 131;
Best Local Similarity 93.9%; Pred. No. 5.4e-55;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      2 MSPAQFLFLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLSDGKTYLNWL 61
          |||||:|||||:|||||
Db      1 MSPAQFLFLVLWIREINGDVVLTQTPLTSLVTIGQPASVCKSSQSLLSDGKTYLNWL 60

Qy     62 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGFHPR 121
          |||||:|||||:|||||
Db     61 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVIYCWQDTHFPD 120

Qy     122 TFGGGTKLEIK 132
          |||||
Db     121 TFGGGTKLEIK 131
```

RESULT 2

```
US-09-647-468-164
; Sequence 164, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence coding for L chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-8
US-09-647-468-164
```

Query Match 93.4%; Score 646; DB 4; Length 131;
Best Local Similarity 93.1%; Pred. No. 1e-54;
Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

```
Qy      2 MSPAQFLFLLVLWIRETNGYVVMQTPTLTLSTVIGQPASISCKSSQSLDSDGKTYLNWL 61
          |||||: || ||:|||||:|||||:|||||:|||||
Db      1 MSPAQFLFLLVLWIRDINGDVVLQTPTLTLSTVIGQPASVSCKSSQSLDSDGKTYLNWL 60

Qy      62 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTFPR 121
          |||||:|||||:|||||:|||||
Db      61 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGYYCWQDTHFPD 120

Qy      122 TFGGGTKLEIK 132
          |||||
Db      121 TFGGGTKLEIK 131
```

RESULT 3

US-09-840-459-102
; Sequence 102, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 102
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-102

Query Match 87.6%; Score 606; DB 4; Length 142;
Best Local Similarity 93.5%; Pred. No. 7.8e-51;
Matches 115; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

```
Qy      10 LLVLWIRETNGYVVMQTPTLTLSTVIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSP 69
          ||||| | |||||:| |||||:|||||
Db      7 LLVLWIRETIGDVVMQTPTLTLSTVGHVPASISCKSSQSLDSDGKTFNWLQRPQGSP 66
```

Qy 70 KRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGYYCWQGTFFPRTFGGGTKL 129
 |||
 Db 67 KRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGYYCWQGTFFPRTFGGGTKL 126

Qy 130 EIK 132
 |||
 Db 127 EIK 129

RESULT 4

US-09-497-625A-102
 ; Sequence 102, Application US/09497625A
 ; Patent No. 6727349
 ; GENERAL INFORMATION:
 ; APPLICANT: LaRosa, Gregory J.
 ; APPLICANT: Horvath, Christopher
 ; APPLICANT: Newman, Walter
 ; APPLICANT: Jones, S. Tarran
 ; APPLICANT: O'Brien, Siobhan H.
 ; APPLICANT: O'Keefe, Theresa
 ; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
 ; TITLE OF INVENTION: METHODS OF USE THEREFOR
 ; FILE REFERENCE: 1855.1052-004
 ; CURRENT APPLICATION NUMBER: US/09/497,625A
 ; CURRENT FILING DATE: 2000-02-03
 ; PRIOR APPLICATION NUMBER: 09/359,193
 ; PRIOR FILING DATE: 1999-07-22
 ; PRIOR APPLICATION NUMBER: 09/121,781
 ; PRIOR FILING DATE: 1998-07-23
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 102
 ; LENGTH: 142
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-497-625A-102

Query Match 87.6%; Score 606; DB 4; Length 142;
 Best Local Similarity 93.5%; Pred. No. 7.8e-51;
 Matches 115; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 10 LLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLLDSGKTYLNWLLQRPQGSP 69
 |||
 Db 7 LLVLWIRETIGDVMTQTPLTSLVTIGVHPASISCKSSQSLLDSGKTYLNWLLQRPQGSP 66

Qy 70 KRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGYYCWQGTFFPRTFGGGTKL 129
 |||
 Db 67 KRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGYYCWQGTFFPRTFGGGTKL 126

Qy 130 EIK 132
 |||
 Db 127 EIK 129

RESULT 5

US-09-203-958A-4
 ; Sequence 4, Application US/09203958A

```
; Patent No. 6682928
; GENERAL INFORMATION:
; APPLICANT: KELER, Tibor
; APPLICANT: GOLDSTEIN, Joel
; APPLICANT: GRAZIANO, Robert
; APPLICANT: DEO, Yashwant M.
; TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR
; TITLE OF INVENTION: BINDING COMPONENTS
; FILE REFERENCE: MXI-099CPA
; CURRENT APPLICATION NUMBER: US/09/203,958A
; CURRENT FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/067232
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-203-958A-4
```

```
Query Match          81.2%; Score 562; DB 4; Length 353;
Best Local Similarity 94.6%; Pred. No. 3.7e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      22 VVMQTPLTTLSTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
          |||||:|||||
Db      177 VVMQTPLTTLSTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPTRLIYLVSKLDS 236

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGFHPRTEFGGGTKLEIK 132
          |||||:|||||
Db      237 GVPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGAHFPQTFFGGGTKLEIK 287
```

RESULT 6

US-09-809-739-11

```
; Sequence 11, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
```

```
; NAME/KEY: SITE
; LOCATION: (1)...(112)
; OTHER INFORMATION: Murine mAb 1D9 light chain variable region
; NAME/KEY: SITE
; LOCATION: (24)...(39)
; OTHER INFORMATION: CDR1
; NAME/KEY: SITE
; LOCATION: (55)...(61)
; OTHER INFORMATION: CDR2
; NAME/KEY: SITE
; LOCATION: (94)...(102)
; OTHER INFORMATION: CDR3
; OTHER INFORMATION: Mouse
US-09-809-739-11
```

```
Query Match          80.9%; Score 560; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.5e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      22 VVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLWLLQRPQGSPKRLIYLVSKLDS 81
          |||||:|||||:|||||
Db      2 VVMTQTPLTSLVTVGHPASISCKSSQSLLDSDGKTFLWLLQRPQGSPKRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTFFPRTFGGGTKLEIK 132
          |||||:|||||:|||||
Db      62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTFFPYTFGGGTKLEIK 112
```

RESULT 7

US-09-840-459-9

```
; Sequence 9, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 112
; TYPE: PRT
```

; ORGANISM: Mus musculus
US-09-840-459-9

Query Match 80.9%; Score 560; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.5e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```
Qy      22 VVMTQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
          |||||:| |||||:|||||
Db      2 VVMTQTPLTLSVTVGHPASISCKSSQSLDSDGKTFLNWLLQRPQSPKRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
          |||||:|||||:|||||
Db      62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPYTFGGGTKLEIK 112
```

RESULT 8

US-09-497-625A-9

; Sequence 9, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-497-625A-9

Query Match 80.9%; Score 560; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.5e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```
Qy      22 VVMTQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDS 81
          |||||:| |||||:|||||
Db      2 VVMTQTPLTLSVTVGHPASISCKSSQSLDSDGKTFLNWLLQRPQSPKRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
          |||||:|||||:|||||
Db      62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPYTFGGGTKLEIK 112
```

RESULT 9

US-09-647-468-149

; Sequence 149, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 149
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of L chain V region of anti-TF mouse
; OTHER INFORMATION: monoclonal antibody ATR-7
US-09-647-468-149

Query Match 80.8%; Score 559; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.9e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
||:|||||||||||||||:|||||||||||||||||||||||||||||||
Db 2 VVLTQTPLTSLVTIGQPASVSCSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61
Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTTHFPRTFGGGTKLEIK 132
|||||||||||||||||||:|||||:|||| |||| |||||
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPDTEFGGGTKLEIK 112

RESULT 10

US-09-647-468-150

; Sequence 150, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850


```
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 150
;   LENGTH: 112
;   TYPE: PRT
;   ORGANISM: Mus sp.
;   FEATURE:
;   OTHER INFORMATION: Amino acid sequence of L chain V region of anti-TF mouse
;   OTHER INFORMATION: monoclonal antibody ATR-8
US-09-647-468-150
```

| | | | |
|----|----|--|-----|
| Qy | 22 | VVMTQTPLTSLVSTIGQPASISCKSSQSLLDSGKTYLNWLLQRPQGSPKRLIYLVSKLDS | 81 |
| | | : : | |
| Db | 2 | VVLTQTPLTSLVSTIGQPASVSKSSQSLLDSGKTYLNWLLQRPQGSPKRLIYLVSKLDS | 61 |
| Qy | 82 | GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGFHFPRTFGGGTKLEIK | 132 |
| | | : | |
| Db | 62 | GVPDRFTGSGSGTDFTLKISRVEAEDLGYYCWQDTHFPDFTFGGGTKLEIK | 112 |

Query Match 80.3%; Score 556; DB 4; Length 112;
Best Local Similarity 92.8%; Pred. No. 3.7e-46;
Matches 103; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

```
Qy      22 VMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
      : :||:|||||
Db      2  IQLTQSPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTFPRTFGGGTKLEIK 132
      |||||
Db      62 GVPDRFTGSGSGTDFTLKISRVEADDLGVYYCWQGTHTFPQTFGGGTKLEIK 112
```

RESULT 12

US-09-497-625A-54

; Sequence 54, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-497-625A-54

Query Match 80.3%; Score 556; DB 4; Length 112;
Best Local Similarity 92.8%; Pred. No. 3.7e-46;
Matches 103; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

```
Qy      22 VMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
      : :||:|||||
Db      2  IQLTQSPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTFPRTFGGGTKLEIK 132
      |||||
Db      62 GVPDRFTGSGSGTDFTLKISRVEADDLGVYYCWQGTHTFPQTFGGGTKLEIK 112
```

RESULT 13

US-08-678-194-6

; Sequence 6, Application US/08678194

```

; Patent No. 5922845
; GENERAL INFORMATION:
;   APPLICANT: Deo, Yashwant M.
;   APPLICANT: Graziano, Robert
;   APPLICANT: Keler, Tibor
;   TITLE OF INVENTION: Therapeutic Multispecific Compounds
;   TITLE OF INVENTION: Comprised of Anti-Fc{SYMBOL 97 \f "Symbol"} Receptor
Antibodi
;   NUMBER OF SEQUENCES: 8
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: LAHIVE & COCKFIELD
;     STREET: 60 State Street, Suite 510
;     CITY: Boston
;     STATE: Massachusetts
;     COUNTRY: USA
;     ZIP: 02109-1875
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/678,194
;     FILING DATE: July 11, 1996
;     PRIOR APPLICATION DATA: No. 5922845e
;     APPLICATION NUMBER: US
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Beth A. Arnold
;     REGISTRATION NUMBER: 35,430
;     REFERENCE/DOCKET NUMBER: MXI-064
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (617)227-7400
;     TELEFAX: (617)227-5941
;   INFORMATION FOR SEQ ID NO: 6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 112 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
US-08-678-194-6

```

```

Query Match          79.2%; Score 548; DB 2; Length 112;
Best Local Similarity 91.0%; Pred. No. 2.2e-45;
Matches 101; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      22 VVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
        : :||:||||:||||||||||||||||||||||||||||||| |||||
Db      2 IQLTQSPLTSLITIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQSPTRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGHFPRTFGGGTKLEIK 132
        |||||:|||||:||||| |||:|||||
Db      62 GVPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGAHFPQTGGGTKLEIK 112

```

```

RESULT 14
US-08-890-011-6

```

```

; Sequence 6, Application US/08890011
; Patent No. 6193966
; GENERAL INFORMATION:
;   APPLICANT: Deo, Yashwant M.
;   APPLICANT: Graziano, Robert
;   APPLICANT: Keler, Tibor
;   TITLE OF INVENTION: Therapeutic Multispecific Compounds
;   TITLE OF INVENTION: Comprised of Anti-Fc
;   TITLE OF INVENTION: {SYMBOL 97 \f "Symbol"} Receptor Antibodies
;   NUMBER OF SEQUENCES: 8
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: LAHIVE & COCKFIELD
;   STREET: 60 State Street, Suite 510
;   CITY: Boston
;   STATE: Massachusetts
;   COUNTRY: USA
;   ZIP: 02109-1875
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/890,011
;   FILING DATE: July 9, 1997
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/678,194
;   FILING DATE: July 11, 1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Jane E. Remillard
;   REGISTRATION NUMBER: 38,872
;   REFERENCE/DOCKET NUMBER: MXI-064CP
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617)227-7400
;   TELEFAX: (617)227-5941
;   INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 112 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-890-011-6

```

```

Query Match          79.2%;  Score 548;  DB 3;  Length 112;
Best Local Similarity 91.0%;  Pred. No. 2.2e-45;
Matches 101;  Conservative 7;  Mismatches 3;  Indels 0;  Gaps 0;

```

```

Qy      22 VVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLWNLLQRPQGSPKRLIYLVSKLDS 81
          : :||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      2  IQLTQSPLTSLITIGQPASISCKSSQSLLDSDGKTYLWNLLQRPQSPTRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGFHPRTFGGGTKLEIK 132
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      62 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGAHFPQTFGGGTKLEIK 112

```

RESULT 15

US-09-262-724-6

; Sequence 6, Application US/09262724

; Patent No. 6303755

; GENERAL INFORMATION:

; APPLICANT: Deo, Yashwant M.

; Graziano, Robert

; Keler, Tibor

; TITLE OF INVENTION: Therapeutic Multispecific Compounds

; Comprised of Anti-Fc{SYMBOL 97 \f "Symbol"}

; Receptor Antibodies

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/262,724

; FILING DATE: 04-Mar-1999

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/678,194

; FILING DATE: July 11, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Beth A. Arnold

; REGISTRATION NUMBER: 35,430

; REFERENCE/DOCKET NUMBER: MXI-064

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 112 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-262-724-6

Query Match 79.2%; Score 548; DB 3; Length 112;

Best Local Similarity 91.0%; Pred. No. 2.2e-45;

Matches 101; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVTIGQPASISCKSSQSLLDS DGKTYLNWLLQRPQSPKRLIYLVSKLDS 81

: :||:||||:|||||||||||||||||||||||||||||||||||||

Db 2 IQLTQSPLTSLITIGQPASISCKSSQSLLDS DGKTYLNWLLQRPQSPTRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGT HFPRTFGGGTKLEIK 132

|||||||||||||||||:|||||:||||| |||:|||||||||

Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGAHFPQTFGGGTKLEIK 112

Search completed: December 13, 2004, 19:19:40
Job time : 28.3778 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 19:04:43 ; Search time 23.4667 Seconds
(without alignments)
541.219 Million cell updates/sec

Title: US-10-010-942B-2
Perfect score: 692
Sequence: 1 MMSPAQFLFLVLVWIRETNG.....CWQGTHTFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|---------------|-------|------------|--------|----|--------|--------------------|
| | | Match | Length | | | |
| 1 | 678 | 98.0 | 132 | 2 | C32513 | Ig kappa chain pre |
| 2 | 587 | 84.8 | 131 | 2 | S31577 | Ig kappa chain m |
| 3 | 566 | 81.8 | 113 | 2 | F30560 | Ig kappa chain V r |
| 4 | 554 | 80.1 | 112 | 2 | A55491 | proteolytic antibo |
| 5 | 548 | 79.2 | 112 | 2 | A36259 | ig kappa chain V r |
| 6 | 547 | 79.0 | 111 | 2 | S20709 | Ig kappa chain V r |
| 7 | 536 | 77.5 | 112 | 2 | PL0273 | Ig kappa chain V r |
| 8 | 516 | 74.6 | 133 | 2 | S42611 | HUNVK protein prec |
| 9 | 515 | 74.4 | 101 | 2 | A33730 | Ig kappa chain V r |
| 10 | 515 | 74.4 | 133 | 2 | S23230 | Ig kappa chain pre |
| 11 | 513 | 74.1 | 142 | 2 | S22902 | Ig kappa chain V r |
| 12 | 512 | 74.0 | 133 | 2 | S40324 | Ig kappa chain V r |
| 13 | 508 | 73.4 | 133 | 1 | K2HURP | Ig kappa chain pre |

| | | | | | | |
|----|-------|------|-----|---|--------|--------------------|
| 14 | 502.5 | 72.6 | 140 | 2 | S22658 | Ig kappa chain pre |
| 15 | 496 | 71.7 | 133 | 1 | A24452 | Ig kappa chain pre |
| 16 | 491 | 71.0 | 132 | 2 | S40322 | Ig kappa chain - h |
| 17 | 485 | 70.1 | 103 | 2 | PH1055 | Ig light chain V r |
| 18 | 476 | 68.8 | 91 | 2 | S42186 | Ig kappa chain V r |
| 19 | 473 | 68.4 | 120 | 2 | S42268 | Ig kappa chain V r |
| 20 | 473 | 68.4 | 120 | 2 | S42267 | Ig kappa chain V r |
| 21 | 470 | 67.9 | 131 | 2 | S09259 | Ig kappa chain pre |
| 22 | 466 | 67.3 | 103 | 2 | PH1056 | Ig light chain V r |
| 23 | 463 | 66.9 | 126 | 2 | S40312 | Ig kappa chain - h |
| 24 | 463 | 66.9 | 131 | 2 | D29380 | Ig kappa chain pre |
| 25 | 462.5 | 66.8 | 131 | 2 | S40355 | Ig kappa chain - h |
| 26 | 462 | 66.8 | 132 | 2 | S26882 | Ig kappa chain V r |
| 27 | 461.5 | 66.7 | 114 | 2 | S49572 | Ig kappa chain pre |
| 28 | 460 | 66.5 | 118 | 2 | S40374 | Ig kappa chain - h |
| 29 | 458.5 | 66.3 | 114 | 2 | B49002 | Ig kappa chain V r |
| 30 | 458 | 66.2 | 131 | 2 | B34904 | Ig kappa chain pre |
| 31 | 458 | 66.2 | 136 | 2 | S40357 | Ig kappa chain V-J |
| 32 | 456 | 65.9 | 112 | 2 | A31807 | Ig kappa chain V r |
| 33 | 456 | 65.9 | 131 | 2 | B39276 | Ig light chain pre |
| 34 | 455 | 65.8 | 132 | 2 | PH0106 | anti-digoxin trans |
| 35 | 454 | 65.6 | 131 | 2 | C34904 | Ig kappa chain pre |
| 36 | 452.5 | 65.4 | 134 | 2 | S40376 | Ig kappa chain - h |
| 37 | 452 | 65.3 | 122 | 2 | S40338 | Ig kappa chain - h |
| 38 | 451 | 65.2 | 128 | 2 | S40373 | Ig kappa chain - h |
| 39 | 450.5 | 65.1 | 130 | 2 | S40321 | Ig kappa chain - h |
| 40 | 450 | 65.0 | 131 | 2 | D34904 | Ig kappa chain pre |
| 41 | 450 | 65.0 | 131 | 2 | B30577 | Ig kappa chain pre |
| 42 | 448 | 64.7 | 131 | 2 | G34903 | Ig kappa chain pre |
| 43 | 448 | 64.7 | 135 | 2 | S40342 | Ig kappa chain - h |
| 44 | 447 | 64.6 | 131 | 2 | B32513 | Ig kappa chain pre |
| 45 | 446 | 64.5 | 115 | 2 | S38715 | Ig kappa chain V r |

ALIGNMENTS

RESULT 1

C32513

Ig kappa chain precursor V region (BXW14) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000

C;Accession: C32513

R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.;

Duchosal, M.A.; Dixon, F.J.; Theofilopoulos, A.N.

J. Clin. Invest. 82, 852-860, 1988

A;Title: Immunoglobulin kappa light chain variable region gene complex organization and immunoglobulin genes encoding anti-DNA autoantibodies in lupus mice.

A;Reference number: A94689; MUID:88331394; PMID:3138286

A;Accession: C32513

A;Molecule type: DNA

A;Residues: 1-132 <KOF>

A;Cross-references: GB:M20830; NID:g196939; PIDN:AAA38844.1; PID:g196940

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 98.0%; Score 678; DB 2; Length 132;
Best Local Similarity 97.7%; Pred. No. 1.6e-51;
Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLSDSGKTYLNW 60
        |||||||
Db      1 MMSPAQFLFLLVLWIRETNGDVVMTQTPLTSLVTIGQPASISCKSSQSLLSDSGKTYLNW 60

Qy      61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTFP 120
        |||||||:|||||:|||||
Db      61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGYYCWQGTHTFP 120

Qy      121 RTFGGGTKLEIK 132
        |||||||
Db      121 RTFGGGTKLEIK 132
```

RESULT 2

S31577

Ig kappa chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

C;Accession: S31577

R;Recinos, A.; Silvey, K.J.; Jensen, R.H.; Stanker, L.H.

submitted to the EMBL Data Library, January 1993

A;Description: Immunoglobulin variable heavy and light chain cDNA sequences for two antidioxin monoclonals.

A;Reference number: S31577

A;Accession: S31577

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-131 <REC>

A;Cross-references: EMBL:Z19575; NID:g53983; PIDN:CAA79627.1; PID:g53984

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 84.8%; Score 587; DB 2; Length 131;
Best Local Similarity 86.3%; Pred. No. 1.1e-43;
Matches 113; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

```
Qy      2 MSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLSDSGKTYLNWL 61
        |||||||:| | | |||||:|||||:| | | |||||
Db      1 MSPAQFLFLLVLSIQEINGDVVMTQAPLTLVTLGQPASISCKSSHSLLSIDGKTYLNWL 60

Qy      62 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTFPR 121
        |||||||:|||||:| | | |||||:| | | |||||
Db      61 LQRPQGSPKRLIYLVSKLDSGVPDRFSGSGSGTDFTLRISRVEAEDLGYYCMQNTHTFPY 120

Qy      122 TFGGGTKLEIK 132
        |||||||:|
Db      121 TFGGGTKLEMK 131
```

RESULT 3

F30560

Ig kappa chain V region (28.4.10A) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
 C;Accession: F30560
 R;Matsuda, T.; Kabat, E.A.
 J. Immunol. 142, 863-870, 1989
 A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclonal antibodies to isomaltosyl oligosaccharides coupled to proteins. T-dependent analogues of alpha(1->6)dextran.
 A;Reference number: A30560; MUID:89110062; PMID:2464028
 A;Accession: F30560
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-113 <MAT>
 A;Cross-references: GB:M24273; NID:g197081; PIDN:AAA63370.1; PID:g197082
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 566; DB 2; Length 113;
 Best Local Similarity 96.4%; Pred. No. 6e-42;
 Matches 107; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
 ||||| ||||||||||||||||||||||||||||||||||||||||||||
 Db 2 VVMTQIPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61
 Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGT HFPRTFGGGTKLEIK 132
 ||||||||||||||||:||||| ||||||||
 Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGT HFPHTFGGGTKLEIK 112

RESULT 4
 A55491
 proteolytic antibody light chain - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
 C;Accession: A55491
 R;Gao, Q.S.; Sun, M.; Tyutyulkova, S.; Webster, D.; Rees, A.; Tramontano, A.; Massey, R.J.; Paul, S.
 J. Biol. Chem. 269, 32389-32393, 1994
 A;Title: Molecular cloning of a proteolytic antibody light chain.
 A;Reference number: A55491; MUID:95096089; PMID:7798238
 A;Accession: A55491
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-112 <GAO>
 A;Cross-references: UNIPROT:Q8K0F8; GB:L34775
 A;Note: authors translated the codon TAT for residue 37 as Thr
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 80.1%; Score 554; DB 2; Length 112;
 Best Local Similarity 94.6%; Pred. No. 6.4e-41;
 Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81

A;Molecule type: DNA

A;Residues: 1-111 <BRE>

A;Cross-references: EMBL:Z11917; NID:g52655; PIDN:CAA77975.1; PID:g52656

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 547; DB 2; Length 111;
Best Local Similarity 92.7%; Pred. No. 2.5e-40;
Matches 102; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
: :||:||||||||||||||||||| |||||||||||||||||||||

Db 2 IQLTQSPLTSLVTIGQPASISCKSSQSLHSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEI 131
|||||||||||||||||:|||||:|||||||||:|||||||

Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPQTFGGGTKLEI 111

RESULT 7

PL0273

Ig kappa chain V region (anti-DNA, D23VK) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004

C;Accession: PL0273

R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.; Weigert, M.

J. Exp. Med. 171, 265-297, 1990

A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.

A;Reference number: PL0231; MUID:90111618; PMID:2104919

A;Accession: PL0273

A;Molecule type: mRNA

A;Residues: 1-112 <SHL>

A;Cross-references: UNIPROT:Q8K0F8

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-23/Region: framework 1

F;16-95/Domain: immunoglobulin homology <IMM>

F;24-39/Region: complementarity-determining 1

F;40-54/Region: framework 2

F;55-61/Region: complementarity-determining 2

F;62-93/Region: framework 3

F;94-102/Region: complementarity-determining 3

F;103-112/Region: framework 4

Query Match 77.5%; Score 536; DB 2; Length 112;
Best Local Similarity 93.7%; Pred. No. 2.3e-39;
Matches 104; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
|||||||||||||||||:|||||:|||||||

Db 2 VVMTQTPLTSLVTIGQPASISCKSSQSLYRNGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
|||||||||||||||||:|||||:|||||

Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCVQGTHFPWTFGGGTKLEIK 112

RESULT 8

S42611

HUNVK protein precursor - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C;Accession: S42611

R;Spatz, L.A.; Williams, M.; Brender, B.; Desai, R.; Latov, N.

J. Neuroimmunol. 36, 29-39, 1992

A;Title: DNA sequence analysis and comparison of the variable heavy and light chain regions of two IgM, monoclonal, anti-myelin associated glycoprotein antibodies.

A;Reference number: S42610; MUID:92138794; PMID:1370957

A;Accession: S42611

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-133 <SPA>

A;Cross-references: EMBL:X54137; NID:g433889; PIDN:CAA38072.1; PID:g433890

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 74.6%; Score 516; DB 2; Length 133;
Best Local Similarity 74.0%; Pred. No. 1.4e-37;
Matches 97; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

```
Qy      1 MMSPAQFLFLLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLW 60
          |  ||| | ||:|:  ::| ||||:|:| | |:|||||:||||: || | ||||
Db      1 MRLPAQLLGLLMLWVPSSGDVMTQSPLSLPVTGLQPASISCRSSQSLVFS DGNTYLNW 60

Qy     61 LLQRPQGSPKRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYC WQGT HFP 120
          |||||:|||| | | |||||:|||||:|||||:||||:|:| || | |:|
Db     61 FQQRPGQSPRRLIYKVSNRD SGVPDRFSGSGTDFTLKISRVEAEDVGIYYC MQGAHWP 120

Qy    121 RTFGGGTKLEI 131
          |||||:|
Db    121 LTFGGGTVKEI 131
```

RESULT 9

A33730

Ig kappa chain V region (1.60) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000

C;Accession: A33730

R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.

Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989

A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unlike genes encoding heavy chains, use variable gene segments dispersed throughout the locus.

A;Reference number: A33730; MUID:89367325; PMID:2505260

A;Accession: A33730

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-101 <LAW>

A;Cross-references: GB:M25996; NID:g197109; PIDN:AAA38911.1; PID:g197110

RESULT 11

S22902

Ig kappa chain V region - human

C;Species: Homo sapiens (man)

C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: S22902

R;Chastagner, P.; Theze, J.; Zouali, M.

Gene 101, 305-306, 1991

A;Title: Cloning of a gene encoding a lupus-associated human autoantibody V(K) region using the polymerase chain reaction and degenerate primers.

A;Reference number: S22902; MUID:91276289; PMID:1905262

A;Accession: S22902

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-142 <CHA>

A;Cross-references: EMBL:X56510

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;47-126/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 513; DB 2; Length 142;
Best Local Similarity 74.0%; Pred. No. 2.7e-37;
Matches 97; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

```
Qy      1 MMSPAQFLFLLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNW 60
          |  ||| | ||:|:  ::| ||||:|:| | |:|||||:||||: ||| ||||
Db      12 MRLPAQLLGLLMLWVPGSSGDVMTQSPLSLPVTLGQPASISCRSSQSLVHSDGNTYLNW 71

Qy      61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTP 120
          |||||:|||| ||  |||||:||||| |||||:||||:||||:| |||:|
Db      72 FQQRPQGSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEADVGVYYCMQGTHTP 131

Qy      121 RTFGGGTKLEI 131
          ||| ||:|
Db      132 FTFGQTRLEI 142
```

RESULT 12

S40324

Ig kappa chain V region - human

C;Species: Homo sapiens (man)

C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004

C;Accession: S40324

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40324

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-133 <KLE>

A;Cross-references: UNIPROT:Q8TCD0; EMBL:X72434

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;33-112/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 512; DB 2; Length 133;
Best Local Similarity 74.4%; Pred. No. 3.1e-37;
Matches 96; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

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Qy      4 PAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQ 63
      ||| | ||:|: ::| ||:|:|:| | ||:| |||||:| ||: ||||| |
Db      1 PAQLLGLLMLWVPGSSGDVVLTSPLSLPVTLGQPASISCRSDQSLVYSDGKTYLNWYQQ 60

Qy     64 RPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGFHPRTF 123
      |||||:|||| || ||||| |||||:|:|:|:|:|:| ||||:| ||
Db     61 RPGQSPRRLIYKVSNRDSGVPDRFTGSGSGTDFTLKISRVEAEDVGYYCMQGFHWPGETF 120

Qy    124 GGGTKLEIK 132
      | |||:|
Db    121 GQGTKVEIK 129
```

RESULT 13

K2HURP

Ig kappa chain precursor V-II region (RPMI) - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004

C;Accession: A01890

R;Klobeck, H.G.; Meindl, A.; Combriato, G.; Solomon, A.; Zachau, H.G.

Nucleic Acids Res. 13, 6499-6513, 1985

A;Title: Human immunoglobulin kappa light chain genes of subgroups II and III.

A;Reference number: A93588; MUID:86041852; PMID:2997711

A;Accession: A01890

A;Molecule type: DNA

A;Residues: 1-133 <KLO>

A;Cross-references: UNIPROT:P06310

A;Note: the sequence was determined from the differentiated gene

C;Genetics:

A;Gene: GDB:IGKV2

A;Cross-references: GDB:136265

A;Map position: 2p12-2p12

A;Introns: 17/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-133/Product: Ig kappa chain V-II region (RPMI) #status predicted <MAT>

F;21-43/Region: framework 1

F;36-115/Domain: immunoglobulin homology <IMM>

F;44-59/Region: complementarity-determining 1

F;60-74/Region: framework 2

F;75-81/Region: complementarity-determining 2

F;82-113/Region: framework 3

F;114-122/Region: complementarity-determining 3

F;123-133/Region: framework 4

F;43-113/Disulfide bonds: #status predicted

Query Match 73.4%; Score 508; DB 1; Length 133;
Best Local Similarity 73.5%; Pred. No. 6.9e-37;

Matches 97; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLDSDGKTYLNW 60
 | ||| | ||:|: ::| ||||:|:| ||:||||||:||||: ||| |||||

Db 1 MRLPAQLLGLLMLWVPSSGDVVMTQSPSLPVTLGQPASISCRSSQSLVSDGNTYLNW 60

Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGFTHF 120
 |||||:|||| || |||||:|||||||:||||:|:| ||||:

Db 61 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGFTHWS 120

Qy 121 RTFGGGTKLEIK 132
 ||| ||:|

Db 121 WTFGQGTKVEIK 132

RESULT 14

S22658

Ig kappa chain precursor V region (0-81VL) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004

C;Accession: S22658

R;Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.

Nucleic Acids Res. 20, 2601, 1992

A;Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-associated idiotype.

A;Reference number: S22657; MUID:92285150; PMID:1598223

A;Accession: S22658

A;Molecule type: mRNA

A;Residues: 1-140 <HIR>

A;Cross-references: UNIPROT:Q8TCD0; EMBL:X59135

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted.<SIG>

F;20-140/Product: Ig kappa chain (fragment) #status predicted <MAT>

F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 72.6%; Score 502.5; DB 2; Length 140;

Best Local Similarity 73.7%; Pred. No. 2.2e-36;

Matches 98; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLDSDGKTYLNW 60
 | ||| | ||:|: ::| ||||:|:| ||:||||||:||||: ||| |||||

Db 1 MRLPAQLLGLLMLWVPSSGDVVMTQSPSLPVTLGQPASISCRSSQSLVHSDGNTYLNW 60

Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGFTHF- 119
 |||||:|||| || |||||:|||||||:||||:|:| ||||:

Db 61 FQQRPGQSPRRLIYRVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQGFTHWS 120

Qy 120 PRTFGGGTKLEIK 132
 | ||| ||:|

Db 121 PITFGQTRLEIK 133

RESULT 15

A24452

Ig kappa chain precursor V-II region (RPMI 6410) - human

C;Species: Homo sapiens (man)

C;Date: 24-Jan-1988 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
 C;Accession: A24452
 R;Weir, L.; Leder, P.
 Nucleic Acids Res. 14, 3957-3970, 1986
 A;Title: Structure and expression of a human subgroup II immunoglobulin kappa gene.
 A;Reference number: A24452; MUID:86232631; PMID:3086847
 A;Accession: A24452
 A;Molecule type: DNA
 A;Residues: 1-133 <WEI>
 A;Cross-references: GB:M36859; NID:g185932; PIDN:AAA58920.1; PID:g185933
 A;Note: this sequence was determined from the differentiated gene
 C;Genetics:
 A;Gene: GDB:IGKV2
 A;Cross-references: GDB:136265
 A;Map position: 2p12-2p12
 A;Introns: 17/1
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-133/Product: Ig kappa chain V-II region (RPMI 6410) #status predicted <MAT>
 F;36-115/Domain: immunoglobulin homology <IMM>
 F;43-113/Disulfide bonds: #status predicted

Query Match 71.7%; Score 496; DB 1; Length 133;
 Best Local Similarity 72.7%; Pred. No. 7.4e-36;
 Matches 96; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

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Qy      1 MMSPAQFLFLVLWIRETNQYVVMQTPTLTLSTIGQPASISCKSSQSLDSDGKTYLNW 60
      |  ||| | || ||:  ::| |||||:||:| ||:|||||||:||||: ||  ||||
Db      1 MRLPAQLLGLRLWVPGSSGDVVMQTSPSLPVTLGQPASISCRSSQSLVYSRNTYLNW 60

Qy      61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTP 120
      |||||:|||| ||  |||||:|||||||:|||||||:||||:|:| |||  |||:
Db      61 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHTS 120

Qy      121 RTFGGGTKLEIK 132
      ||| |||:|||
Db      121 WTFGQGTKVEIK 132
  
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Search completed: December 13, 2004, 19:18:39
 Job time : 25.4667 secs

OM protein - protein search, using sw model

Run on: December 13, 2004, 19:17:53 ; Search time 94.8444 Seconds
(without alignments)
497.104 Million cell updates/sec

Title: US-10-010-942B-2
Perfect score: 692
Sequence: 1 MMSPAQFLFLLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|---------------|-------|----------------|--------|----|-------------------|-------------------|
| 1 | 692 | 100.0 | 132 | 14 | US-10-010-942B-2 | Sequence 2, Appli |
| 2 | 692 | 100.0 | 132 | 15 | US-10-388-389-2 | Sequence 2, Appli |
| 3 | 692 | 100.0 | 132 | 16 | US-10-703-713-2 | Sequence 2, Appli |
| 4 | 692 | 100.0 | 132 | 16 | US-10-704-070-2 | Sequence 2, Appli |
| 5 | 650 | 93.9 | 135 | 9 | US-09-881-823-10 | Sequence 10, Appl |
| 6 | 649 | 93.8 | 131 | 15 | US-10-462-062-163 | Sequence 163, App |
| 7 | 646 | 93.4 | 131 | 15 | US-10-462-062-164 | Sequence 164, App |
| 8 | 640 | 92.5 | 132 | 14 | US-10-010-942B-5 | Sequence 5, Appli |
| 9 | 640 | 92.5 | 132 | 15 | US-10-388-389-5 | Sequence 5, Appli |
| 10 | 640 | 92.5 | 132 | 16 | US-10-703-713-5 | Sequence 5, Appli |
| 11 | 640 | 92.5 | 132 | 16 | US-10-704-070-5 | Sequence 5, Appli |
| 12 | 636 | 91.9 | 132 | 13 | US-10-006-773-11 | Sequence 11, Appl |
| 13 | 630 | 91.0 | 132 | 14 | US-10-010-942B-11 | Sequence 11, Appl |
| 14 | 630 | 91.0 | 132 | 15 | US-10-388-389-11 | Sequence 11, Appl |
| 15 | 630 | 91.0 | 132 | 16 | US-10-703-713-11 | Sequence 11, Appl |
| 16 | 630 | 91.0 | 132 | 16 | US-10-704-070-11 | Sequence 11, Appl |
| 17 | 606 | 87.6 | 142 | 9 | US-09-840-459-102 | Sequence 102, App |
| 18 | 606 | 87.6 | 142 | 16 | US-10-766-773-102 | Sequence 102, App |
| 19 | 606 | 87.6 | 142 | 16 | US-10-766-610-102 | Sequence 102, App |
| 20 | 606 | 87.6 | 142 | 16 | US-10-733-563-102 | Sequence 102, App |
| 21 | 562 | 81.2 | 353 | 10 | US-09-203-958A-4 | Sequence 4, Appli |
| 22 | 560 | 80.9 | 112 | 9 | US-09-835-087-1 | Sequence 1, Appli |
| 23 | 560 | 80.9 | 112 | 9 | US-09-809-739-11 | Sequence 11, Appl |
| 24 | 560 | 80.9 | 112 | 9 | US-09-840-459-9 | Sequence 9, Appli |
| 25 | 560 | 80.9 | 112 | 16 | US-10-766-773-9 | Sequence 9, Appli |
| 26 | 560 | 80.9 | 112 | 16 | US-10-766-610-9 | Sequence 9, Appli |
| 27 | 560 | 80.9 | 112 | 16 | US-10-733-563-9 | Sequence 9, Appli |
| 28 | 560 | 80.9 | 122 | 15 | US-10-272-899A-86 | Sequence 86, Appl |
| 29 | 560 | 80.9 | 130 | 15 | US-10-272-899A-88 | Sequence 88, Appl |
| 30 | 559 | 80.8 | 112 | 15 | US-10-462-062-149 | Sequence 149, App |
| 31 | 559 | 80.8 | 112 | 15 | US-10-462-062-150 | Sequence 150, App |
| 32 | 556 | 80.3 | 112 | 9 | US-09-840-459-54 | Sequence 54, Appl |
| 33 | 556 | 80.3 | 112 | 16 | US-10-766-773-54 | Sequence 54, Appl |
| 34 | 556 | 80.3 | 112 | 16 | US-10-766-610-54 | Sequence 54, Appl |
| 35 | 556 | 80.3 | 112 | 16 | US-10-733-563-54 | Sequence 54, Appl |
| 36 | 551 | 79.6 | 500 | 14 | US-10-168-809-22 | Sequence 22, Appl |
| 37 | 548 | 79.2 | 112 | 9 | US-09-772-120-6 | Sequence 6, Appli |
| 38 | 548 | 79.2 | 535 | 9 | US-09-968-851-38 | Sequence 38, Appl |
| 39 | 547 | 79.0 | 162 | 14 | US-10-410-907A-30 | Sequence 30, Appl |
| 40 | 546 | 78.9 | 112 | 14 | US-10-323-903-1 | Sequence 1, Appli |
| 41 | 538 | 77.7 | 112 | 9 | US-09-835-087-5 | Sequence 5, Appli |
| 42 | 538 | 77.7 | 112 | 9 | US-09-809-739-16 | Sequence 16, Appl |
| 43 | 538 | 77.7 | 112 | 9 | US-09-840-459-14 | Sequence 14, Appl |
| 44 | 538 | 77.7 | 112 | 16 | US-10-766-773-14 | Sequence 14, Appl |
| 45 | 538 | 77.7 | 112 | 16 | US-10-766-610-14 | Sequence 14, Appl |

ALIGNMENTS

RESULT 1
 US-10-010-942B-2
 ; Sequence 2, Application US/10010942B
 ; Publication No. US20030165496A1

```
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-010-942B-2
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Query Match          100.0%; Score 692; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 5.4e-57;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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Qy      1 MMSPAQFLFLVLWIRETNGYVVMQTQPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MMSPAQFLFLVLWIRETNGYVVMQTQPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60

Qy     61 LLQRPQGSPKRLIYLVS KLDSGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGT HFP 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LLQRPQGSPKRLIYLVS KLDSGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGT HFP 120

Qy    121 RTFGGGTKLEIK 132
      |||||||||||
Db    121 RTFGGGTKLEIK 132
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RESULT 2

US-10-388-389-2

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; Sequence 2, Application US/10388389
; Publication No. US2004008777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-388-389-2

Query Match 100.0%; Score 692; DB 15; Length 132;
Best Local Similarity 100.0%; Pred. No. 5.4e-57;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW 60
|||||
Db 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW 60

Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGT HFP 120
|||||
Db 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGT HFP 120

Qy 121 RTFGGGTKLEIK 132
|||||
Db 121 RTFGGGTKLEIK 132

RESULT 3

US-10-703-713-2

; Sequence 2, Application US/10703713
; Publication No. US20040171815A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/703,713
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-703-713-2

Query Match 100.0%; Score 692; DB 16; Length 132;
Best Local Similarity 100.0%; Pred. No. 5.4e-57;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
          |||
Db      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60

Qy     61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFP 120
          |||
Db     61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFP 120

Qy    121 RTFGGGTKLEIK 132
          |||
Db    121 RTFGGGTKLEIK 132
```

RESULT 4

US-10-704-070-2

; Sequence 2, Application US/10704070
; Publication No. US20040171816A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/704,070
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)

US-10-704-070-2

Query Match 100.0%; Score 692; DB 16; Length 132;
Best Local Similarity 100.0%; Pred. No. 5.4e-57;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
          |||
Db      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60

Qy     61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFP 120
          |||
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Db 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGT HFP 120
 Qy 121 RTFGGGTKLEIK 132
 |||||
 Db 121 RTFGGGTKLEIK 132

RESULT 5

US-09-881-823-10
 ; Sequence 10, Application US/09881823
 ; Patent No. US20020068066A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SHI, WENYUAN
 ; APPLICANT: ANDERSON, MAXWELL
 ; APPLICANT: MORRISON, SHERIE
 ; APPLICANT: TRINH, RYAN
 ; APPLICANT: WIMS, LETITIA
 ; APPLICANT: CHEN, LI
 ; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
 ; FILE REFERENCE: 22851-032
 ; CURRENT APPLICATION NUMBER: US/09/881,823
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: US 07/378,577
 ; PRIOR FILING DATE: 1999-08-20
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 135
 ; TYPE: PRT
 ; ORGANISM: Murine
 US-09-881-823-10

Query Match 93.9%; Score 650; DB 9; Length 135;
 Best Local Similarity 93.2%; Pred. No. 4.7e-53;
 Matches 123; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSGKTYLNW 60
 |||||
 Db 1 MMSPAQFLFLLVLWIRETNGDVVMQTPLTSLVTIGQPASISCKSSQSLLDRDGRYLSW 60
 Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGT HFP 120
 |||||
 Db 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGT HFP 120
 Qy 121 RTFGGGTKLEIK 132
 ||| |||||
 Db 121 LTFGAGTKLELK 132

RESULT 6

US-10-462-062-163
 ; Sequence 163, Application US/10462062
 ; Publication No. US20040044187A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SATO, KOH
 ; APPLICANT: ADACHI, HIDEKI
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)


```
; TITLE OF INVENTION:  AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
; FILE REFERENCE: 053466-0360
; CURRENT APPLICATION NUMBER: US/10/462,062
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino
acid
; OTHER INFORMATION: sequence for L chain V region of anti-TF mouse monoclonal
; OTHER INFORMATION: antibody ATR-7
US-10-462-062-163
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```
Query Match          93.8%;  Score 649;  DB 15;  Length 131;
Best Local Similarity 93.9%;  Pred. No. 5.7e-53;
Matches 123;  Conservative 4;  Mismatches 4;  Indels 0;  Gaps 0;
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Qy      2 MSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWL 61
          |||:|||||
Db      1 MSPAQFLFLLVLWIREINGDVVLTQTPLTSLVTIGQPASVSCSSQSLDSDGKTYLNWL 60

Qy      62 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGFTHFPR 121
          |||:|||||
Db      61 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPD 120

Qy      122 TFGGGTKLEIK 132
          |||
Db      121 TFGGGTKLEIK 131
```

RESULT 7

```
US-10-462-062-164
; Sequence 164, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
; TITLE OF INVENTION:  AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
; FILE REFERENCE: 053466-0360
; CURRENT APPLICATION NUMBER: US/10/462,062
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
```

```
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino
acid
; OTHER INFORMATION: sequence for L chain V region of anti-TF mouse monoclonal
; OTHER INFORMATION: antibody ATR-8
US-10-462-062-164
```

```
Query Match          93.4%; Score 646; DB 15; Length 131;
Best Local Similarity 93.1%; Pred. No. 1.1e-52;
Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      2 MSPAQFLFLLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWL 61
        |||||: || ||:|||||:|||||:|||||
Db      1 MSPAQFLFLLVLWIRDINGDVVLTQTPLTSLVTIGQPASVSCKSSQSLLDSDGKTYLNWL 60

Qy     62 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTFPR 121
        |||||:|||||:|||||
Db     61 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPD 120

Qy     122 TFGGGTKLEIK 132
        |||||
Db     121 TFGGGTKLEIK 131
```

RESULT 8

US-10-010-942B-5

```
; Sequence 5, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-010-942B-5
```

```
Query Match          92.5%; Score 640; DB 14; Length 132;
Best Local Similarity 90.2%; Pred. No. 4e-52;
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;
```

```

Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLSDGKTYLW 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MMSPAQFLFLLVLWIRETNGYVVMQTSPLSLPVTPGEPASISCKSSQSLLSDGKTYLW 60

Qy      61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGT HFP 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 LLQKPGQSPQRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGT HFP 120

Qy      121 RTFGGGTKLEIK 132
        |||| |||:|||
Db      121 RTFGQGTKVEIK 132

```

RESULT 9

US-10-388-389-5

```

; Sequence 5, Application US/10388389
; Publication No. US2004008777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-388-389-5

```

```

Query Match          92.5%; Score 640; DB 15; Length 132;
Best Local Similarity 90.2%; Pred. No. 4e-52;
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLSDGKTYLW 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MMSPAQFLFLLVLWIRETNGYVVMQTSPLSLPVTPGEPASISCKSSQSLLSDGKTYLW 60

Qy      61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGT HFP 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 LLQKPGQSPQRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGT HFP 120

Qy      121 RTFGGGTKLEIK 132
        |||| |||:|||

```



```

; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/704,070
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-704-070-5

```

```

Query Match          92.5%; Score 640; DB 16; Length 132;
Best Local Similarity 90.2%; Pred. No. 4e-52;
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTQPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MMSPAQFLFLLVLWIRETNGYVVMQSPLSLPVTPGEPASISCKSSQSLLDSDGKTYLNW 60

Qy      61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGT HFP 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 LLQKPGQSPQRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDVGVYYCWQGT HFP 120

Qy      121 RTFGGGTKLEIK 132
        |||| |||:|||
Db      121 RTFGQGTKVEIK 132

```

```

RESULT 12
US-10-006-773-11

```

```

; Sequence 11, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against
Tumor Antigens
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1

```

```
; SEQ ID NO 11
;   LENGTH: 132
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-10-006-773-11
```

Query Match 91.9%; Score 636; DB 13; Length 132;
Best Local Similarity 93.9%; Pred. No. 9.4e-52;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

```
Qy      2 MSPAQFLFLVLVWIRETNGYVVMQTPTLTL SVTIGQPASISCKSSQSLLDSDGKTYLNWL 61
      |||:|||||
Db      1 MSPAQFLFLVLVWIQETNGDVVMQTPTLTL SVTIGQPASISCKSSQSLLYSNGKTYLNWL 60
```

Qy 62 LQRPGQSPKRLIYLVSKLDSGVPDRFTGS GSGTDFTLKISRIEAEDLGLYYC WQGTHFPR 121
| | | | | : | | | | |
Db 61 LQRPGQSPKRLIYLVSKLDSGVPDRFTGS GSGTDFTLKIS RVEAEDLG VVYC WQGTHFPH 120

Qy 122 TFGGGTKLEIK 132
 |||||
 Db 121 TFGGGTKLEIK 131

RESULT 13

US-10-010-942B-11

; Sequence 11, Application US/10010942B

; Publication No. US20030165496A1

; GENERAL INFORMATION:

; APPLICANT: Basi, Gurig

; APPLICANT: Saldanha, Jose

; APPLICANT: Yednock, Ted

; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE

; TITLE OF INVENTION: BETA AMYLOID PEPTIDE

; FILE REFERENCE: ELN-002

; CURRENT APPLICATION NUMBER: US/10/010,942B

; CURRENT FILING DATE: 2002-12-06

; PRIOR APPLICATION NUMBER: US 60/251,892

; PRIOR FILING DATE: 2000-12-06

; NUMBER OF SEQ ID NOS: 63

```
; SOFTWARE: FastSEQ for Windows Version 4.0
```

; SEQ ID NO 11

```
; LENGTH: 132
```

```
; TYPE: PRT
```

; ORGANISM: Artificial Sequence

; FEATURE:

```
; NAME/KEY: SIGNAL
```

; LOCATION: (1)...(20)

; OTHER INFORMATION: humanized 3D6 light chain variable region

US-10-010-942B-11

Query Match 91.0%; Score 630; DB 14; Length 132;
Best Local Similarity 89.4%; Pred. No. 3.4e-51;
Matches 118; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLLDSGKTYLNW 60
|||||:|:| | |:|||||

Db 1 MMSPAQFLFLVLWIRETNGDVMTQSPSLPVTGPGEASISCKSSQSLLDSGKTYLNW 60

Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFP 120
 |||:||||:||||||||||||||||||:||||||||||||||:||||:|:|||||||
 Db 61 LLQKPGQSPQRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTTHFP 120

Qy 121 RTFGGGTKLEIK 132
 |||| |||:|||
 Db 121 RTFGQGTKVEIK 132

RESULT 14

US-10-388-389-11
 ; Sequence 11, Application US/10388389
 ; Publication No. US2004008777A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Basi, Guriq
 ; APPLICANT: Saldanha, Jose
 ; APPLICANT: Yednock, Ted
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
 ; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
 ; FILE REFERENCE: ELN-002CP
 ; CURRENT APPLICATION NUMBER: US/10/388,389
 ; CURRENT FILING DATE: 2003-03-12
 ; PRIOR APPLICATION NUMBER: US 10/010,942
 ; PRIOR FILING DATE: 2001-12-06
 ; PRIOR APPLICATION NUMBER: US 60/251,892
 ; PRIOR FILING DATE: 2000-12-06
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 11
 ; LENGTH: 132
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: SIGNAL
 ; LOCATION: (1)...(20)
 ; OTHER INFORMATION: humanized 3D6 light chain variable region
 US-10-388-389-11

Query Match 91.0%; Score 630; DB 15; Length 132;
 Best Local Similarity 89.4%; Pred. No. 3.4e-51;
 Matches 118; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLW 60
 |||||||||||||||| ||||:|:| || |:|||||||||||||||||||
 Db 1 MMSPAQFLFLLVLWIRETNGDVMTQSPLSLPVTGPGEPAISCKSSQSLLDSDGKTYLW 60

Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFP 120
 |||:||||:||||||||||||||||||:||||||||||||||:||||:|:|||||||
 Db 61 LLQKPGQSPQRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTTHFP 120

Qy 121 RTFGGGTKLEIK 132
 |||| |||:|||
 Db 121 RTFGQGTKVEIK 132

RESULT 15

US-10-703-713-11
; Sequence 11, Application US/10703713
; Publication No. US20040171815A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/703,713
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-703-713-11

Query Match 91.0%; Score 630; DB 16; Length 132;
Best Local Similarity 89.4%; Pred. No. 3.4e-51;
Matches 118; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLLDSDGKTYLNW 60
|||||:|:| || |:|||||
Db 1 MMSPAQFLFLLVLWIRETNGDVVMTQSPLSLPVTTPGEPASISCKSSQSLLDSDGKTYLNW 60
Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHTFP 120
|||:||||:|||||:|||||:||||:|:|||||
Db 61 LLQKPGQSPQRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHTFP 120
Qy 121 RTFGGGTKLEIK 132
|||| |||:|
Db 121 RTFGQGTKVEIK 132

Search completed: December 13, 2004, 19:34:49
Job time : 95.8444 secs

OM protein - protein search, using sw model

Run on: December 13, 2004, 18:50:06 ; Search time 125.644 Seconds
(without alignments)
604.479 Million cell updates/sec

Title: US-10-010-942B-2
Perfect score: 692
Sequence: 1 MMSPAQFLFLLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| % | | | | | | | |
|--------|-------|-------|--------|----|------------|-------------|-------------|
| Result | Query | | | | | | |
| No. | Score | Match | Length | DB | ID | Description | |
| 1 | 611 | 88.3 | 148 | 2 | Q8K122 | Q8k122 | mus musculu |
| 2 | 583 | 84.2 | 239 | 2 | Q8K0F8 | Q8k0f8 | mus musculu |
| 3 | 511 | 73.8 | 239 | 2 | Q8TCD0 | Q8tcd0 | homo sapien |
| 4 | 508 | 73.4 | 133 | 1 | KV2F_HUMAN | P06310 | homo sapien |
| 5 | 471 | 68.1 | 239 | 2 | Q6P491 | Q6p491 | homo sapien |
| 6 | 471 | 68.1 | 239 | 2 | Q8NEK0 | Q8nek0 | homo sapien |
| 7 | 471 | 68.1 | 239 | 2 | AAH63599 | Aah63599 | homo sapi |
| 8 | 460 | 66.5 | 238 | 2 | Q99M37 | Q99m37 | mus musculu |
| 9 | 459 | 66.3 | 238 | 2 | Q8VCI6 | Q8vci6 | mus musculu |
| 10 | 453 | 65.5 | 239 | 2 | Q8VC55 | Q8vc55 | mus musculu |
| 11 | 448 | 64.7 | 239 | 2 | BAC04905 | Bac04905 | homo sapi |
| 12 | 444.5 | 64.2 | 114 | 2 | Q9UL80 | Q9ul80 | homo sapien |
| 13 | 441.5 | 63.8 | 240 | 2 | Q6PIH6 | Q6pih6 | homo sapien |
| 14 | 441.5 | 63.8 | 240 | 2 | AAH34142 | Aah34142 | homo sapi |
| 15 | 436 | 63.0 | 114 | 2 | AAR11017 | Aar11017 | mus muscu |

| | | | | | | |
|----|-------|------|-----|---|------------|--------------------|
| 16 | 434 | 62.7 | 113 | 1 | KV2G_MOUSE | P01631 mus musculu |
| 17 | 417 | 60.3 | 117 | 1 | KV2E_HUMAN | P06309 homo sapien |
| 18 | 415 | 60.0 | 113 | 1 | KV2D_HUMAN | P01617 homo sapien |
| 19 | 414.5 | 59.9 | 115 | 1 | KV2A_HUMAN | P01614 homo sapien |
| 20 | 414 | 59.8 | 113 | 1 | KV2B_HUMAN | P01615 homo sapien |
| 21 | 411 | 59.4 | 105 | 2 | AAR11074 | Aar11074 mus muscu |
| 22 | 408.5 | 59.0 | 104 | 2 | AAR11056 | Aar11056 mus muscu |
| 23 | 406 | 58.7 | 104 | 2 | AAR11064 | Aar11064 mus muscu |
| 24 | 405 | 58.5 | 104 | 2 | AAR11024 | Aar11024 mus muscu |
| 25 | 398 | 57.5 | 104 | 2 | Q9JL82 | Q9jl82 mus musculu |
| 26 | 398 | 57.5 | 109 | 2 | AAR10990 | Aar10990 mus muscu |
| 27 | 397 | 57.4 | 104 | 2 | AAR11063 | Aar11063 mus muscu |
| 28 | 394 | 56.9 | 102 | 2 | AAR11040 | Aar11040 mus muscu |
| 29 | 389.5 | 56.3 | 112 | 1 | KV2C_HUMAN | P01616 homo sapien |
| 30 | 388 | 56.1 | 113 | 1 | KV2F_MOUSE | P01630 mus musculu |
| 31 | 386 | 55.8 | 129 | 1 | KV3L_HUMAN | P18135 homo sapien |
| 32 | 381 | 55.1 | 112 | 2 | Q6LEM8 | Q6lem8 mus musculu |
| 33 | 381 | 55.1 | 112 | 2 | BAD00151 | Bad00151 mus muscu |
| 34 | 380.5 | 55.0 | 134 | 1 | KV4C_HUMAN | P06314 homo sapien |
| 35 | 380 | 54.9 | 113 | 1 | KV2E_MOUSE | P03976 mus musculu |
| 36 | 377.5 | 54.6 | 236 | 2 | Q6PIL8 | Q6pil8 homo sapien |
| 37 | 377.5 | 54.6 | 236 | 2 | AAH32451 | Aah32451 homo sapi |
| 38 | 376 | 54.3 | 235 | 2 | Q6GMV9 | Q6gmv9 homo sapien |
| 39 | 374 | 54.0 | 112 | 1 | KV2D_MOUSE | P01629 mus musculu |
| 40 | 374 | 54.0 | 120 | 1 | KV2B_MOUSE | P01627 mus musculu |
| 41 | 373.5 | 54.0 | 131 | 1 | KV3I_MOUSE | P01661 mus musculu |
| 42 | 373 | 53.9 | 113 | 1 | KV2C_MOUSE | P01628 mus musculu |
| 43 | 373 | 53.9 | 129 | 1 | KV3M_HUMAN | P18136 homo sapien |
| 44 | 373 | 53.9 | 133 | 1 | KV4B_HUMAN | P06313 homo sapien |
| 45 | 369.5 | 53.4 | 240 | 2 | Q6PJB5 | Q6pjb5 homo sapien |

ALIGNMENTS

RESULT 1

Q8K122

ID Q8K122 PRELIMINARY; PRT; 148 AA.

AC Q8K122;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Hypothetical protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Salivary gland;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC028925; AAH28925.1; -.
 DR HSSP; Q8K0F8; 1KN2.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 148 AA; 16345 MW; 183920BBD9F3B521 CRC64;

Query Match 88.3%; Score 611; DB 2; Length 148;
 Best Local Similarity 97.5%; Pred. No. 3.8e-51;
 Matches 116; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWL 61
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||
 Db 1 MSPAQFLFLVLWIRETNGDVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWL 60
 Qy 62 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGLYCYWQGTHTFP 120
 ||||||||||||||||||| ||||||||||||||||||| |||||||:|||||:|||||
 Db 61 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYCYWQGTHTFP 119

RESULT 2

Q8K0F8

ID Q8K0F8 PRELIMINARY; PRT; 239 AA.
 AC Q8K0F8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=mix FVB/N;


```
Qy      61 LLQRPGQSPKRLIYLVS KLDSGVPDRFTGSGSGTDFTLKISR IEAEDLG LY YCWQGTHFP 120
       ||||||| : ||||| : ||||| : ||| | |||
Db      61 LLQRPGQSPKRLISLVS KLDSGVPDRFSGSGTDFTLKISRVEAEDLGVYYCLQSTHFP 120

Qy     121 RTFGGGTKLEIK 132
       |||||||
Db     121 YTFGGGTKLEIK 132
```

RESULT 3

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Q8TCD0
ID Q8TCD0 PRELIMINARY; PRT; 239 AA.
AC Q8TCD0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC022362; AAH22362.1; -.
DR PIR; S22658; S22658.
DR PIR; S34095; S34095.
DR PIR; S40324; S40324.
DR PIR; S40374; S40374.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.

```

DR HSSP; P01834; 1I7Z.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 1.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;

Query Match 73.8%; Score 511; DB 2; Length 239;
 Best Local Similarity 72.7%; Pred. No. 3.2e-41;
 Matches 96; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNQYVVMQTPLTLSTIGQPASISCKSSQSLDSDGKTYLNW 60
 | ||| | ||: ||: : : | ||||: ||: | ||: ||||| : ||: ||| |||||
 Db 1 MRLPAQLLGLLMLWVPGSSGDVVMQSPSLPVTLGQPASISCRSTQSLVYSDGNTYLNW 60
 Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCQGTTHFP 120
 ||||| : |||| | | ||||| : ||||| ||||| : ||: ||| : ||: | ||| : |
 Db 61 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGTDFTLKITRVEAEDVGVYFCMQGTHWP 120
 Qy 121 RTFGGGTKLEIK 132
 ||| |||||
 Db 121 STFGQGTKLEIK 132

RESULT 4

KV2F_HUMAN

ID KV2F_HUMAN STANDARD; PRT; 133 AA.
 AC P06310;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region RPMI 6410 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86041852; PubMed=2997711;
 RA Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
 RT "Human immunoglobulin kappa light chain genes of subgroups II and
 RT III.";
 RL Nucleic Acids Res. 13:6499-6513(1985).

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 CC or send an email to license@isb-sib.ch).

```

CC -----
DR EMBL; Z00020; CAA77315.1; -.
DR PIR; A01890; K2HURP.
DR HSSP; Q99M37; 1I9I.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL      1      20
FT CHAIN       21     133      Ig kappa chain V-II region RPMI 6410.
FT DOMAIN     21      43      Framework-1.
FT DOMAIN     44      59      Complementarity-determining-1.
FT DOMAIN     60      74      Framework-2.
FT DOMAIN     75      81      Complementarity-determining-2.
FT DOMAIN     82     113      Framework-3.
FT DOMAIN    114     122      Complementarity-determining-3.
FT DOMAIN    123     132      Framework-4.
FT DISULFID    43     113      By similarity.
FT NON_TER    133     133
SQ SEQUENCE   133 AA;  14707 MW;  513CCAF3673009EE CRC64;

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Query Match          73.4%;  Score 508;  DB 1;  Length 133;
Best Local Similarity 73.5%;  Pred. No. 3.2e-41;
Matches 97;  Conservative 16;  Mismatches 19;  Indels 0;  Gaps 0;

```

```

Qy      1 MMSPAQFLFLVLWIRETNQYVVMQTPTLTLSTIGQPASISCKSSQSLDSDGKTYLNW 60
      | ||| | ||:| :||| |||:| ||:|||||||:||||: ||| |||||
Db      1 MRLPAQLLGLLMLWVPSSGDVVMQTSPSLPVTLGQPASISCRSSQSLVYSDGNTYLNW 60

Qy     61 LLQRPQGSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCQGTHFP 120
      |||||:|||| || |||||:|||||||:||||:|:| ||| |||:
Db     61 FQQRPGQSPRRLIYKVSNRDGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWS 120

Qy    121 RTFGGGTKLEIK 132
      ||| |||:|
Db    121 WTFGQGTKVEIK 132

```

RESULT 5

Q6P491

```

ID   Q6P491          PRELIMINARY;      PRT;   239 AA.
AC   Q6P491;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.

```

RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC063599; AAH63599.1; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 1.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;

Query Match 68.1%; Score 471; DB 2; Length 239;

Best Local Similarity 68.8%; Pred. No. 2.4e-37;

Matches 88; Conservative 21; Mismatches 19; Indels 0; Gaps 0;

Qy 5 AQFLFLLVLWIRETNQYVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQR 64
 || | ||:||: ::| :|||||||: ||:|||||||:|:| || |:| |||:| |
 Db 5 AQLLGLLMLWVPGSSGDIVMTQTPLSSPVTLGQPASISCRSSESLLSNGNTYLSWLHQR 64
 Qy 65 PGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTFFPRTFG 124
 ||| |:| ||| :| |||||:|:|:|||||||:|:|:|:| | :| |||||
 Db 65 PGQPPRLIYKISNRFSGVPDRFSGGAGTDFTLKISRVEAEDVGVYYCMQVSHFPRTFG 124
 Qy 125 GGTKLEIK 132
 ||:| |||

RESULT 6

Q8NEK0

ID Q8NEK0 PRELIMINARY; PRT; 239 AA.
AC Q8NEK0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC030814; AAH30814.1; -.
DR PIR; S23638; S23638.
DR PIR; S34091; S34091.
DR PIR; S40342; S40342.
DR PIR; S40357; S40357.
DR HSSP; P01834; 1I7Z.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.

DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 68.1%; Score 471; DB 2; Length 239;
Best Local Similarity 68.2%; Pred. No. 2.4e-37;
Matches 90; Conservative 19; Mismatches 23; Indels 0; Gaps 0;

QY 1 MMSPAQFLFLVLWIRETNGYVVMQTPTLSVTIGQPASISCKSSQSLLDSDGKTYLNW 60
| ||| | ||:|: :| :|||:|:| || |:| ||||:| |||| | ||:|
Db 1 MRLPAQLLGLLMLWVSGSSGDIVMTQSPLSLPVTTPGEPASISCRSSQSLLHSDGYNLYLDW 60

QY 61 LLQRPQGSPKRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCQWQTHFP 120
||:||||: ||| | |||||:|||||||:| |||:|:| || |
Db 61 YLQKPGQSPQLLIYLGSNRASGVDPDRFSGSGTDFTLKISKVEAEDVGIYYCMQGLQTP 120

QY 121 RTFGGGTKLEIK 132
: ||| |||: |||
Db 121 QTFGQGTKVEIK 132

RESULT 7

AAH63599

ID AAH63599 PRELIMINARY; PRT; 239 AA.
AC AAH63599;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC063599; AAH63599.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;

Query Match 68.1%; Score 471; DB 2; Length 239;
 Best Local Similarity 68.8%; Pred. No. 2.4e-37;
 Matches 88; Conservative 21; Mismatches 19; Indels 0; Gaps 0;

Qy 5 AQFLFLLVLWIRETNGYVVMQTPTLSVTIGQPASISCKSSQSLSDSGKTYLNWLLQR 64
 || | ||: ||: :: | : || || || | : ||: || || || || | : | ||: || ||
 Db 5 AQLLGLLMLWVPGSSGDIVMTQTPLSSPVTLGQPASISCRSSESLHLSNGNTYLSWLHQR 64
 Qy 65 PGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCQWQTHFPRTFG 124
 || | | : || | : | || || || | : ||: || || || || | : ||: || | : || || || ||
 Db 65 PGQPPRLLIYKISNRFSGVDPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQVSHFPRTFG 124
 Qy 125 GGTKLEIK 132
 ||: || ||
 Db 125 QGTRVEIK 132

RESULT 8

Q99M37

ID Q99M37 PRELIMINARY; PRT; 238 AA.
 AC Q99M37;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=mix FVB/N;
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=mix FVB/N;
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC002035; AAH02035.1; -.
 DR PIR; A31807; A31807.
 DR PIR; A32248; A32248.
 DR PIR; B32248; B32248.
 DR PIR; C32248; C32248.
 DR PIR; D28195; D28195.
 DR PIR; E28195; E28195.
 DR PIR; F27887; F27887.
 DR PIR; F32530; F32530.
 DR PIR; JL0029; JL0029.
 DR PIR; PH1035; PH1035.
 DR PIR; PH1036; PH1036.
 DR PIR; PH1037; PH1037.
 DR PIR; PH1038; PH1038.
 DR PIR; PH1039; PH1039.
 DR PIR; PH1040; PH1040.
 DR PIR; PH1042; PH1042.
 DR PIR; PH1043; PH1043.
 DR PIR; PH1044; PH1044.
 DR PIR; S07455; S07455.
 DR PIR; S16112; S16112.
 DR PIR; S24498; S24498.
 DR PIR; S24500; S24500.
 DR PIR; S24501; S24501.
 DR PIR; S24502; S24502.
 DR PIR; S24503; S24503.
 DR PIR; S24504; S24504.
 DR PIR; S24506; S24506.
 DR PIR; S24507; S24507.
 DR PIR; S24508; S24508.
 DR PIR; S24509; S24509.
 DR PIR; S24510; S24510.
 DR PIR; S24529; S24529.
 DR PIR; S24530; S24530.
 DR PIR; S24531; S24531.
 DR PIR; S24532; S24532.
 DR PIR; S24533; S24533.
 DR PIR; S24534; S24534.
 DR PIR; S24535; S24535.
 DR PIR; S24536; S24536.
 DR PIR; S24537; S24537.
 DR PIR; S24538; S24538.
 DR PIR; S24539; S24539.
 DR PDB; 1I9I; X-ray; L=20-238.

DR PDB; 1I9J; X-ray; L=20-238.
 DR PDB; 1KTR; X-ray; L=17-132.
 DR PDB; 1LO2; X-ray; L/X=20-238.
 DR PDB; 1LO3; X-ray; L/X=20-238.
 DR PDB; 1LO4; X-ray; L=20-236.
 DR PDB; 2MPA; X-ray; L=20-238.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 1.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 66.5%; Score 460; DB 2; Length 238;
 Best Local Similarity 69.6%; Pred. No. 2.7e-36;
 Matches 87; Conservative 17; Mismatches 21; Indels 0; Gaps 0;

QY 8 LFLVLVWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQG 67
 | :|: || :: |||||:| |::| ||||:||||: |:| ||| | ||:| |
 Db 7 LLVLMFWIPASSSDVVMQTPTLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQ 66
 QY 68 SPKRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGTHFPRTFGGGT 127
 ||| ||| || |||||:|||||:|||||:||||:|:| | ||| ||
 Db 67 SPKLLIYKVS NRFS GVPDRFSGSGSGTDFTLKISRVEAEDLG VYYCFQGSHPVPTFGSGT 126
 QY 128 KLEIK 132
 |||||
 Db 127 KLEIK 131

RESULT 9

Q8VCI6

ID Q8VCI6 PRELIMINARY; PRT; 238 AA.
 AC Q8VCI6;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC019760; AAH19760.1; -.
 DR PIR; A27887; A27887.
 DR PIR; A32248; A32248.
 DR PIR; A33933; A33933.
 DR PIR; B27887; B27887.
 DR PIR; B30577; B30577.
 DR PIR; B31485; B31485.
 DR PIR; B32248; B32248.
 DR PIR; B41940; B41940.
 DR PIR; C27887; C27887.
 DR PIR; C32248; C32248.
 DR PIR; C34904; C34904.
 DR PIR; D27887; D27887.
 DR PIR; D29380; D29380.
 DR PIR; E28833; E28833.
 DR PIR; E32530; E32530.
 DR PIR; F32530; F32530.
 DR PIR; H31485; H31485.
 DR PIR; PH0106; PH0106.
 DR PIR; PH1030; PH1030.
 DR PIR; PH1031; PH1031.
 DR PIR; PH1034; PH1034.
 DR PIR; PH1045; PH1045.
 DR PIR; PL0257; PL0257.
 DR PIR; PT0178; PT0178.
 DR PIR; PT0359; PT0359.
 DR PIR; S07455; S07455.
 DR PIR; S16112; S16112.
 DR PIR; S26334; S26334.
 DR PIR; S53750; S53750.
 DR PIR; S60066; S60066.
 DR PDB; 1A3R; X-ray; L=-.
 DR PDB; 1ACY; X-ray; L=-.
 DR PDB; 1H3P; X-ray; L=20-238.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.

DR Pfam; PF07654; C1-set; 1.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match 66.3%; Score 459; DB 2; Length 238;
 Best Local Similarity 70.4%; Pred. No. 3.4e-36;
 Matches 88; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

QY 8 LFLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQG 67
 | :|: || :: |||||:| |:| ||||:||||: |:| |||:| ||:|
 Db 7 LLVLMFWIPASSDVMTQTPLSLPVS LGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQ 66
 QY 68 SPKRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGT HFPRTFGGGT 127
 ||| ||| || |||||:|||||:|||||:|||||: |:| | | | |||||
 Db 67 SPKLLIYKVS NRFSGVDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPTFGGGT 126
 QY 128 KLEIK 132
 |||||
 Db 127 KLEIK 131

RESULT 10

Q8VC55

ID Q8VC55 PRELIMINARY; PRT; 239 AA.
 AC Q8VC55;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC021781; AAH21781.1; -.
 DR PIR; A33933; A33933.
 DR PDB; 1KC5; X-ray; L=21-239.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 1.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;

Query Match 65.5%; Score 453; DB 2; Length 239;
 Best Local Similarity 67.4%; Pred. No. 1.3e-35;
 Matches 89; Conservative 16; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLDSDGKTYLNW 60
 | | : ||: :: ||:|||||:| | | | |||||:||||:| | | |
 Db 1 MKLPVLLVLLVLLFTSPASSSDVLTQTPLSLPVNIGDQASISCKSTKSLNSDGFTYLDW 60
 Qy 61 LLQRPQGSPKRLIYLVSKLDGSGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQTHFP 120
 ||:|||||: ||||| | |||||:|||||||:|||||:| | | |
 Db 61 YLQKPGQSPQLLIYLVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQSNHLP 120
 Qy 121 RTFGGGTKLEIK 132
 |||||
 Db 121 YTFGGGTKLEIK 132

RESULT 11

BAC04905

ID BAC04905 PRELIMINARY; PRT; 239 AA.
 AC BAC04905;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE CDNA FLJ39619 fis, clone SMINT2000984, highly similar to IG KAPPA
 DE CHAIN V-II REGION GM607.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Small intestine;

RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 DR EMBL; AK096938; BAC04905.1; -.
 SQ SEQUENCE 239 AA; 25964 MW; 78D9005B0E5CA51E CRC64;

Query Match 64.7%; Score 448; DB 2; Length 239;
 Best Local Similarity 64.4%; Pred. No. 4e-35;
 Matches 85; Conservative 21; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNGYVVM TQTPLTSLVTIGQPASISCKSSQSLLDS DGKTYL NW 60
 | ||| | ||:| :| :||| :||| | | | :||| :||| | :| | :|
 Db 1 MRLPAQLLGLLMLWVSGSSGEIVMTQSPLSLPVTAGEPASISCRSSQSLLHSNGYNYVDW 60
 Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGT HFP 120
 ||:||||| :||| | | ||||| :||| ||| ||||| :||| :| | |
 Db 61 YLQKPGQSPQLLIFLSSNRASGVPDRFSGSGSGTDFILKISRVEAEDVG VYFCMQALQMP 120
 Qy 121 RTFGGGTKLEIK 132
 ||| |||:|
 Db 121 GTFGQGTKVEIK 132

RESULT 12

Q9UL80

ID Q9UL80 PRELIMINARY; PRT; 114 AA.

AC Q9UL80;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035034; AAD56270.1; -.
 DR PIR; B49002; B49002.
 DR PIR; S23638; S23638.
 DR PIR; S34094; S34094.
 DR PIR; S34095; S34095.
 DR HSSP; Q99M37; 1I9I.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 1
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 64.2%; Score 444.5; DB 2; Length 114;
 Best Local Similarity 76.8%; Pred. No. 3.8e-35;
 Matches 86; Conservative 12; Mismatches 13; Indels 1; Gaps 1;

QY 22 VVMTQTPLTSLVITIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLLIYLVSKLDS 81
 |||||:|:| ||: |||||:|||| : ||| ||||| |||||:|||| || ||
 Db 2 VVMTQSPLSLPVTLRQPASISCRSSQSPVYSDGNTYLNWFQQRPQGSPRRLIYKVSNRDS 61
 QY 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTFPR-TFGGGTKLEIK 132
 |||||:|||||:|||||:||||:| ||| |||:|
 Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDVGYYCMQGTHTWPPWTFGQGTKVEIK 113

RESULT 13

Q6PIH6

ID Q6PIH6 PRELIMINARY; PRT; 240 AA.
 AC Q6PIH6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE IGKV1-5 protein.
 GN Name=IGKV1-5;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RESULT 14

AAH34142

ID AAH34142 PRELIMINARY; PRT; 240 AA.
 AC AAH34142;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC034142; AAH34142.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 240 AA; 26234 MW; 188D4DD8BB781EC4 CRC64;

Query Match 63.8%; Score 441.5; DB 2; Length 240;
 Best Local Similarity 66.2%; Pred. No. 1.7e-34;
 Matches 88; Conservative 17; Mismatches 27; Indels 1; Gaps 1;

Qy 1 MMSPAQFLFLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLDSDGKTYLW 60
 | ||| | ||:||: ::| :|| |::| ||| |::| |||:| ||| | :| | :|
 Db 1 MRLPAQLLGLLMLWVSGSSGDIVMAQSPLSLSVTPGEPASISCRSSQSLHLSNGYNYFDW 60
 Qy 61 LLQRPQGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTF- 119

```

      ||:||||: || | |||||:|||||||:||||:|:|| |
Db      61 YLQKPGQSPQLLIYWGSGNRASGVDPDRFSGSGTDFTLKISRVEAEDVGVIYCMQALQTP 120

Qy      120 PRTFGGGTKLEIK 132
      | ||| |||||
Db      121 PYTFGQGTKLEIK 133

```

RESULT 15

AAR11017

```

ID  AAR11017    PRELIMINARY;      PRT;    114 AA.
AC  AAR11017;
DT  02-MAR-2004 (TrEMBLrel. 27, Created)
DT  02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT  02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE  ANA immunoglobulin kappa light chain (Fragment).
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=B6.Sle1; TISSUE=Spleen;
RA  Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT  "Antinuclear autoantibodies from B6.Sle1 mice.";
RL  Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; AY436857; AAR11017.1; -.
FT  NON_TER      1      1
FT  NON_TER      114     114
SQ  SEQUENCE     114 AA;  12422 MW;  C94A4DDCF55E8A8C CRC64;

```

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Query Match          63.0%; Score 436; DB 2; Length 114;
Best Local Similarity 75.2%; Pred. No. 2.5e-34;
Matches 82; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

```

```

Qy      24 MTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDSGV 83
      |||||:| |::| |||||:||||:| |:| ||| | ||:||||| ||| || |||
Db      1 MTQTPLSLPVS LGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVS NRFSGV 60

Qy      84 PDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGT HFPRTFGGGTKLEIK 132
      ||||:|||||||:|||||:||||:|:| | |||||
Db      61 PDRFSGSGSGTDFTLKISRVEAEDLGVIYCFQGSHPVPTFGGGTKLEIK 109

```

Search completed: December 13, 2004, 19:17:44
Job time : 127.644 secs